

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:52:35 ; Search time 15 Seconds  
(without alignments)  
57.681 Million cell updates/sec

Title: US-09-878-603-14

Perfect score: 47

Sequence: 1 KYKHSVVK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	18	38.3	9	2 PT0231	Ig heavy chain CDR
2	17	36.2	6	2 S11556	hydrogensulfite re
3	16	34.0	9	2 I46016	cytochrome P-450
4	15	31.9	8	2 T14906	hypothetical prote
5	15	31.9	9	2 S13889	phosphoenolpyruvat
6	14	29.8	6	2 JN0861	peptidyl-di-peptida
7	14	29.8	6	2 A61140	sperm acrosomal pr
8	14	29.8	9	2 C36730	hutu protein - kle
9	13	27.7	3	3 A60898	burstin - chicken
10	13	27.7	6	2 S11024	hydrogensulfite re
11	13	27.7	7	2 JN0859	peptidyl-di-peptida
12	13	27.7	7	2 PT0246	Ig heavy chain CDR
13	13	27.7	8	2 XGHUEU	urine glycopeptide
14	13	27.7	8	2 S16324	hypothetical prote
15	13	27.7	8	2 A59028	MHC class I histoc
16	12	27.7	9	2 S78426	52.5K protein - sp
17	12	25.5	5	2 I40698	biotin B - Citrob
18	12	25.5	5	2 T10954	hypothetical prote
19	12	25.5	5	2 P00689	photosystem I 10.4
20	12	25.5	6	2 S02617	alcohol dehydrogen
21	12	25.5	7	1 NYPG7	hypothalamic hepta
22	12	25.5	7	2 P00663	membrane protein -
23	12	25.5	7	2 A15398	choline oxidase (E
24	12	25.5	7	2 S17976	glucose isomerase
25	12	25.5	7	2 S78024	ribosomal protein
26	12	25.5	7	4 I56695	hypothetical L2 pr
27	12	25.5	8	2 S63493	dissimilatory sulf
28	12	25.5	8	2 S68802	nitrate reductase
29	12	25.5	8	2 J50316	leucokinin VI - Ma

## ALIGNMENTS

### RESULT 1

PT0231

Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0231

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0231

A:Molecule type: DNA

A:Residues: 1-9 <YAK>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 38.3%; Score 18; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YKHS 5

Db 1 YTHS 4

### RESULT 2

S11556

hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragmen

N:Alternate names: bisulfite reductase; desulfosulfidin

C:Species: Desulfovibrio thermophilus

C:Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998

C:Accession: S11556

R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.

Biochim. Biophys. Acta 1040, 112-118, 1990

A:Title: Purification and characterization of bisulfite reductase (desulfosulfidin) f

A:Reference number: S11024; MUID:90335276; PMID:2165817

A:Accession: S11556

A:Molecule type: prctein

A:Residues: 1-6 <FAU>

C:Keywords: oxidoreductase

Query Match 36.2%; Score 17; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYK 3

Db 4 KYK 6

### RESULT 3

I46016

cytokeatin 4 - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 05-Nov-1999  
 C:Accession: I46016  
 R:Blessing, M.; Jorcano, J.L.; Franke, W.W.  
 EMBO J. 8, 117-126, 1989  
 A:Title: Enhancer elements directing cell-type-specific expression of cytokeatin genes  
 A:Reference number: I46016; MUID:892331609; PMID:2469572  
 A:Accession: I46016  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-9 <BLE>  
 A:Cross-references: EMBL:X14478; NID:g303; PIDN:CAA32640.1; PID:g577897

Query Match 34.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSV 6  
 || : ||  
 Db 3 YKSTV 7

RESULT 4  
 T14906  
 hypothetical protein - parsley  
 C:Species: Petroselinum crispum (parsley)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14906  
 R:Feidbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Welsshaar, B.  
 Plant Cell 6, 1607-1621, 1994  
 A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator  
 A:Reference number: Z18259; MUID:95128172; PMID:7827494  
 A:Accession: T14906  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <PFL>  
 A:Cross-references: EMBL:S75395; NID:g913201; PID:el94245

Query Match 31.9%; Score 15; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHSV 6  
 || : ||  
 Db 2 KHTL 5

RESULT 5  
 S13889  
 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize  
 C:Species: Zea mays (maize)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
 C:Accession: S13889  
 R:Jiao, J.; Choillet, R.  
 Arch. Biochem. Biophys. 283, 300-305, 1990  
 A:Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase  
 A:Reference number: S13889; MUID:91112741; PMID:2148863  
 A:Accession: S13889  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <JIA>  
 C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 31.9%; Score 15; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HSV 6  
 || : ||  
 Db 2 HSI 4

RESULT 6  
 JN0861  
 peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito  
 C:Species: Sarda orientalis (striped bonito)  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C:Accession: JN0861  
 R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory  
 A:Reference number: JN0859; MUID:94080036; PMID:7764272  
 A:Accession: JN0861  
 A:Molecule type: protein  
 A:Residues: 1-6 <MAT>  
 A:Experimental source: liver  
 C:Comment: The carboxyl end is essential for the protein's expression of angiotensin  
 C:Superfamily: bradykinin-potentiating peptide  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.8%; Score 14; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKH 4  
 || : ||  
 Db 3 YPH 5

RESULT 7  
 A61140  
 sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)  
 C:Species: Urechis caupo  
 C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-Apr-1994  
 C:Accession: A61140  
 R:Gould, M.C.; Stephano, J.L.  
 Dev. Biol. 146, 509-518, 1991  
 A:Title: Peptides from sperm acrosomal protein that initiate egg development.  
 A:Reference number: A61140; MUID:91323672; PMID:1864468  
 A:Accession: A61140  
 A:Molecule type: protein  
 A:Residues: 1-6 <GOU>

Query Match 29.8%; Score 14; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VVK 9  
 || : ||  
 Db 1 VAK 4

RESULT 8  
 C36730  
 hutU protein - Klebsiella pneumoniae (fragment)  
 C:Species: Klebsiella pneumoniae  
 C>Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 08-Oct-1999  
 C:Accession: C36730  
 R:Schwacha, A.; Bender, R.A.  
 J. Bacteriol. 172, 5477-5481, 1990  
 A:Title: Nucleotide sequence of the gene encoding the repressor for the histidine uti  
 A:Reference number: A36730; MUID:90366611; PMID:2203754  
 A:Accession: C36730  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-9 <SCH>  
 A:Cross-references: GB:M34604; NID:g149203; PIDN:AAA25076.1; PID:g149206

Query Match 29.8%; Score 14; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
 || : ||  
 Db 5 KYR 7

## RESULT 9

A60898  
bursin - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A60898  
R:Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.  
Science 231, 997-999, 1986  
A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the bursa of Fabricius  
A:Reference number: A60898; MUID:86122916; PMID:3484838  
A:Accession: A60898  
A:Molecule type: protein  
A:Residues: 1-3 <AUD>  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hormone  
F:3/Modified site: amidated carboxyl end (Gly). #status experimental

Query Match 27.7%; Score 13; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KH 4  
| |  
Db 1 KH 2

## RESULT 10

S11024  
hydrogensulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: bisulfite reductase; desulfosulfide  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: S11024

R:Pauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; L.  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfosulfide) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817  
A:Accession: S11024  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
C:Keywords: oxidoreductase

Query Match 27.7%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
| |  
Db 4 KFK 6

## RESULT 11

JN0859  
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito  
C:Species: Sarda orientalis (striped bonito)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: JN0859  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
A:Reference number: JN0859; MUID:94080036; PMID:7764272  
A:Accession: JN0859  
A:Molecule type: protein  
A:Residues: 1-7 <MAT>

A:Experimental source: intestine  
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 27.7%; Score 13; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 SVVK 8  
| | |  
Db 1 SVAK 4

## RESULT 12

PT0246  
Ig heavy chain CDR3 region (clone 2-103D) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0246  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0246  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 27.7%; Score 13; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSVV 7  
| |  
Db 1 HEVL 4

## RESULT 13

XGHUEU  
urine glycopeptide - human  
C:Species: Homo sapiens (man)  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A03188  
R:Lote, C.J.; Weiss, J.B.  
Biochem. J. 123, 25F, 1971  
A:Title: Identification in urine of a low-molecular-weight polar glycopeptide contain  
A:Reference number: A03188; MUID:72062338; PMID:5126885  
A:Accession: A03188  
A:Molecule type: protein  
A:Residues: 1-8 <LOT>  
C:Comment: The identity of the glycoprotein from which this peptide is derived is unk  
re has also been found (see FIR:XGHUE).

C:Superfamily: unassigned animal peptides  
C:Keywords: glycoprotein  
F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHS 5  
| |  
Db 2 EHS 4

## RESULT 14

S16324  
hypothetical protein 2 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C:Accession: S16324  
R:Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A:Title: A novel class of plant proteins containing a homeodomain with a closely link  
A:Reference number: S16323; MUID:91266907; PMID:1675603  
A:Accession: S16324  
A:Status: translation not shown  
A:Molecule type: mRNA

A:Residues: 1-8 <RUB>  
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3  
DB 2 EYK 4

RESULT 15  
A59028  
MHC class I histocompatibility antigen HLA-C alpha chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 31-Dec-2001  
C:Accession: A59028  
R:Escolano, J.M.  
Submitted to the Protein Sequence Database, August 1998  
A:Reference number: A59028  
A:Accession: A59028  
A:Molecule type: protein  
A:Residues: 1-8 <ESC>  
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

Query Match 27.7%; Score 13; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKHSVVKK 9  
DB 1 YFYTAVSR 8

Search completed: January 29, 2003, 09:54:43  
Job time : 16 secs

GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: January 29, 2003, 09:47:08 : Search time 11 Seconds  
(without alignments)  
33.935 Million cell updates/sec

Title: US-09-878-603-14  
Perfect score: 47  
Sequence: 1 KYKHSVKK 9

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 231

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	15	31.9	7	1 FAR2_ASCSU	P31890 ascaris suu
2	15	31.9	9	1 ULAD_HUMAN	P31929 homo sapien
3	14	29.8	9	1 HUTU_KLEAE	P12381 klebsiella
4	13	27.7	8	1 FUSS_FUSSO	P81010 fusarium so
5	13	27.7	8	1 GLUR_HUMAN	P02729 homo sapien
6	13	27.7	9	1 BUK_CLOPA	P81337 clostridium
7	13	27.7	9	1 FARP_CALSI	P38495 callinectes
8	13	27.7	9	1 NSK1_SARBU	P41492 sarcophaga
9	12	25.5	5	1 BIOB_CITFR	P12997 citrobacter
10	12	25.5	6	1 OVM_LEPDE	P42985 leptinotars
11	12	25.5	7	1 CHOX_ALCSP	P16101 alcalligenes
12	12	25.5	7	1 FAFS_HIRME	P42564 hirudo medi
13	12	25.5	7	1 HV7_PIG	P01153 sus scrofa
14	12	25.5	8	1 ANG2_BOTJA	Q10582 bothrops ja
15	12	25.5	8	1 LCK4_LEUMA	P21143 leucophaea
16	12	25.5	8	1 LCK6_LEUMA	P19988 leucophaea
17	12	25.5	8	1 UF06_MOUSE	P38644 mus musculu
18	11	23.4	9	1 FAFS_PANRE	P82661 panagrellus
19	11	23.4	9	1 LPCA_STAAU	P38684 staphylococ
20	11	23.4	9	1 TAL1_PICJA	P17440 pichia jadi
21	11	23.4	9	1 XYLA_STRSQ	P19149 streptomyce
22	10	21.3	7	1 FAR1_ASCSU	P31889 ascaris suu
23	10	21.3	8	1 ACT_CARMA	P80709 carcinus ma
24	10	21.3	8	1 AL16_CARMA	P81819 carcinus ma
25	10	21.3	9	1 NEF_HVIZ8	P12481 human immun
26	10	21.3	9	1 NEUX_HUMAN	P04277 homo sapien
27	9	19.1	3	1 THYL_PIG	P01151 sus scrofa
28	9	19.1	4	1 FYR1_ATEL	P58706 anthopleura
29	9	19.1	5	1 EI03_LITRU	P82099 lithoria rub
30	9	19.1	5	1 FARP_ARTTR	P41853 artiopesthi
31	9	19.1	6	1 PRC1_PERAM	P01373 periplaneta
32	9	19.1	6	1 TRP1_PSEPU	P36414 pseudomonas
33	9	19.1	7	1 EI05_LITRU	P82101 lithoria rub

34	9	19.1	7	1 UC24_MAIZE	P80630 zea mays (m
35	9	19.1	8	1 B44K_PORGI	P81886 porphyromon
36	9	19.1	8	1 CAD1_ENTFA	P13268 enterococcu
37	9	19.1	8	1 UC26_MAIZE	P80632 zea mays (m
38	9	19.1	9	1 MOSH_CLIJA	P19852 clypeaster
39	9	19.1	9	1 PGLR_DIAAB	P81179 diaprepes a
40	9	19.1	9	1 PKL1_PERAM	P82691 periplaneta
41	9	19.1	9	1 ULAK_MOUSE	P99031 mus musculu
42	9	19.1	9	1 UP47_HUMAN	P30093 homo sapien
43	8	17.0	3	1 GRW4_HUMAN	P01157 homo sapien
44	8	17.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
45	8	17.0	4	1 DCML_PSECH	P19916 pseudomonas

## ALIGNMENTS

RESULT 1  
FAR2\_ASCSU STANDARD; PRT; 7 AA.  
ID FAR2\_ASCSU STANDARD; PRT; 7 AA.  
AC P31890:  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE FMRamide-like neuropeptide AF2.  
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides), and  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253, 6233;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=A. suum;  
RX MEDLINE=93324431; PubMed=8332542;  
RT Cowden C., Stretton A.O.W.;  
RA "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";  
RL Peptides 14:42:-430(1993).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P. redivivus;  
RX MEDLINE=95060998; PubMed=7970891;  
RA Maule A.G., Shaw C., Bowman J.W.;  
RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the  
RT free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";  
RL Parasitology 109:351-356(1994).  
CC -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.  
CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 31.9%; Score 15; DB 1; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.1e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KHSVVK 8  
|| :  
Db 1 KHEYLK 6

RESULT 2  
ULAD\_HUMAN STANDARD; PRT; 9 AA.  
ID ULAD\_HUMAN STANDARD; PRT; 9 AA.  
AC P31929:  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
DR SWISS-2DPAGE; P31929; HUMAN.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match 31.9%; Score 15; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VVKK 9
DB 1 LVKK 4

RESULT 3
HUTU_KLEAF
ID HUTU_KLEAF STANDARD; PRT; 9 AA.
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hut(P) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90368611; PubMed=2203754;
RA Schwacha A., Bender R.A.;
RT "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -!- CATALYTIC ACTIVITY: 4,5-dihydro-4-oxo-5-imidazolepropanoate =
CC urocanate + H(2)O.
CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; M19665; AAA25078.1; -
DR EMBL; M34604; AAA25076.1; -
DR PIR; C36730; C36730.
DR InterPro; IPR000193; Urocanase.
DR PROSITE; PS01233; UROCANASE; PARTIAL.

KW Histidine metabolism; Lyase; NAD.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 29.8%; Score 14; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYK 3
DB 5 KYR 7

RESULT 4
FUSS_FUSSO
ID FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON_TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HSV 6
DB 5 HNV 7

RESULT 5
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25P-25P(1971).
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
CC PIR: A03188; XGHUEU.
DR Glycoprotein.
KW CARBOHYD
FT NON_TER 1
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;

```

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHS 5

DB 2 EHS 4

# RESULT 6

BUK\_CLOPA  
ID BUK\_CLOPA STANDARD; PRT; 9 AA.  
AC P81337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).  
GN BUK.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5.  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flensburg R., Skjelvald L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -1- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl  
phosphate to butyrate (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + 2-butanolate -> ADP + butanoyl phosphate.  
CC -1- PATHWAY: Involved in the acidogenic phase of fermentation.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE ACETOKINASE FAMILY.  
DR InterPro: IPR000890; Acetate\_kin.  
DR PROSITE: PS01075; ACETATE\_KINASE\_1; PARTIAL.  
DR PROSITE: PS01076; ACETATE\_KINASE\_2; PARTIAL.  
DR KW Transferase; Kinase.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 27.7%; Score 13; DB 1; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1.1e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 YKHSV 7  
DB 2 YKLLI 7

Query Match 27.7%; Score 13; DB 1; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1.1e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKHSV 7

DB 2 YKLLI 7

# RESULT 7

FARP\_CALSI  
ID FARP\_CALSI STANDARD; PRT; 9 AA.  
AC P38435;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FWRamide-like neuropeptide.  
OS Callinectes sapidus (Blue crab).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;  
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.  
OX NCBI\_TaxID=6763;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270479; PubMed=1815216;  
RA Krajniak K.G.;  
RT "The identification and structure-activity relations of a  
cardioactive FWRamide-related peptide from the blue crab Callinectes  
sapidus".  
RL Peptides 12:1295-1302(1991).  
CC -1- FUNCTION: CARDIOACTIVE PEPTIDE.  
CC -1- SIMILARITY: BELONGS TO THE FARP (FWRAMIDE RELATED PEPTIDE)

CC Neuropeptide; Amidation.  
KW MOD\_RES 9 AA; 1159 MW; 134F0729D5A4045B CRC64;  
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match 27.7%; Score 13; DB 1; Length 9;  
Best Local Similarity 28.6%; Pred. No. 1.1e+05;  
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKHSV 8

DB 2 YNRSFLR 8

# RESULT 8

NSKI\_SARBU  
ID NSKI\_SARBU STANDARD; PRT; 9 AA.  
AC P41492;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Neosulfakinin-I (NEB-SK-I).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RX MEDLINE=93083101; PubMed=1360367;  
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
RT "Isolation and primary structure of two sulfakinin-like peptides from  
the fleshfly, Neobellieria bullata".  
RL Comp. Biochem. Physiol. 103C:135-142(1992).  
CC -1- FUNCTION: MYOTROPIC PEPTIDE.  
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
DR InterPro: IPR001651; Gastrin.  
DR PROSITE: PS00259; GASTRIN; 1.  
DR KW Neuropeptide; Amidation; Sulfation.  
FT MOD\_RES 4 4  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;

Query Match 27.7%; Score 13; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKH 4

DB 4 YGH 6

# RESULT 9

BIOB\_CITFR  
ID BIOB\_CITFR STANDARD; PRT; 5 AA.  
AC P12997;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).  
GN BIOB.  
OS Citrobacter freundii.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Citrobacter.  
OX NCBI\_TaxID=546;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89006280; PubMed=2971595;  
RA Shivan D., Campbell A.;  
RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
Citrobacter freundii and Salmonella typhimurium biotin operons.";  
RL Gene 67:203-211(1988).

```

CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -!- PATHWAY: Biotin biosynthesis; last step.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPIC ACID SYNTHETASES
CC FAMILY.
CC -----
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CC -----
CC EMBL: M21922; -: NOT-ANNOTATED_CDS.
CC DR Biotin biosynthesis; Iron-sulfur; Transferase.
CC KW
CC FT NON_TER 5
CC SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HS 5
Db 3 HS 4

RESULT 10
OVM_LEPDE STANDARD; PRT; 6 AA.
ID OVM_LEPDE AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM).
OS Leptinotarsa decemlineata. (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
OC NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head.
RX MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RL decemlineata.";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC KW
CC KW Neuropeptide; Amidation.
CC FT MOD_RES 6
CC SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YK 3
Db 3 YK 4

RESULT 11
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID CHOX_ALCSP AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)

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DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyde + H(2)O(2).
CC DR PIR; A15398; A15398.
CC KW Oxidoreductase.
CC FT NON_TER 7
CC SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HS 5
Db 5 HS 6

RESULT 12
FAR5_HIRME STANDARD; PRT; 7 AA.
ID FAR5_HIRME AC P42564;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GGYMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OC NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC KW Neuropeptide; Amidation.
CC FT MOD_RES 7
CC SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KY 2
Db 3 KY 4

RESULT 13
HY7_PIG STANDARD; PRT; 7 AA.
ID HY7_PIG AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

```



RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=81213980; PubMed=6263778;  
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,  
 RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;  
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro  
 RT ACTH-releasing activity from porcine hypothalamus";  
 RL Horm. Metab. Res. 13:228-232(1981).  
 DR PIR; A01417; NYPG7.  
 SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HS 5  
 ||  
 Db 4 HS 5

## RESULT 14

ANG2\_BOTJA STANDARD; PRT; 8 AA.  
 AC Q10582;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide II (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR Interpro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 25.5%; Score 12; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKH 4  
 ||  
 Db 4 YIH 6

## RESULT 15

LCK4\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21143;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin IV (L-IV).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
 OC Blaberoidea; Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]

RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides  
 RT from Leucophaea maderae: members of a new family of  
 RT Cephalomyotropins";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 25.5%; Score 12; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HS 5  
 ||  
 Db 5 HS 6

Search completed: January 29, 2003, 09:53:47  
 Job time : 13 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:51:53 ; Search time 28 Seconds  
(without alignments)  
66.229 Million cell updates/sec

Title: US-09-878-603-14  
Perfect score: 47  
Sequence: 1 KYKHSVVK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 686

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_protein.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	46.8	8	Q05403	Q05403 saccharomyc
2	18	38.3	8	P87488	P87488 oncorhynch
3	18	38.3	9	Q9UC36	Q9UC36 homo sapien
4	17	36.2	8	Q15894	Q15894 homo sapien
5	17	36.2	8	Q34909	Q34909 locusta mig
6	16	34.0	7	Q91182	Q91182 gnatholebia
7	16	34.0	8	Q9BY15	Q9BY15 gnatholebia
8	16	34.0	8	Q9BFA0	Q9BFA0 macaca mulia
9	16	34.0	8	Q9BF99	Q9BF99 hylobates c
10	16	34.0	9	Q28093	Q28093 bos taurus
11	16	34.0	9	Q99MG3	Q99MG3 mus musculu
12	15	31.9	8	Q56429	Q56429 thermus the
13	14	29.8	9	Q95GN1	Q95GN1 pelargonium
14	14	29.8	9	Q92766	Q92766 canine dist
15	14	29.8	9	Q91LX6	Q91LX6 macaca neme
16	13	27.7	5	Q99007	Q99007 hordeum vul

17	13	27.7	7	2	P72081	P72081 nocardia la
18	13	27.7	7	12	Q66205	Q66205 transmissib
19	13	27.7	8	2	Q45615	Q45615 bacillus su
20	13	27.7	8	2	P81158	P81158 anabaena sp
21	13	27.7	8	6	Q9XS11	Q9XS11 canis famli
22	13	27.7	8	12	Q9E8Q7	Q9E8Q7 beet soli-b
23	13	27.7	8	12	Q9E8Q6	Q9E8Q6 beet soli-b
24	13	27.7	8	12	Q9DSN6	Q9DSN6 beet soli-b
25	13	27.7	8	12	Q9E8Q5	Q9E8Q5 beet soli-b
26	13	27.7	8	12	Q9E8Q4	Q9E8Q4 beet soli-b
27	13	27.7	8	12	Q9DSN5	Q9DSN5 beet soli-b
28	13	27.7	8	12	Q9E8Q3	Q9E8Q3 beet soli-b
29	13	27.7	8	12	Q9DSN4	Q9DSN4 beet soli-b
30	13	27.7	8	12	Q9DSN3	Q9DSN3 beet soli-b
31	13	27.7	8	12	Q9DSN2	Q9DSN2 beet soli-b
32	13	27.7	8	12	Q9E8Q2	Q9E8Q2 beet soli-b
33	13	27.7	8	12	Q9E8Q1	Q9E8Q1 beet soli-b
34	13	27.7	8	12	Q9DSN1	Q9DSN1 beet soli-b
35	13	27.7	8	12	Q9DSN0	Q9DSN0 beet soli-b
36	13	27.7	8	12	Q9E8Q0	Q9E8Q0 beet soli-b
37	13	27.7	8	12	Q9E8P9	Q9E8P9 beet soli-b
38	13	27.7	8	12	Q9E8P8	Q9E8P8 beet soli-b
39	13	27.7	8	12	Q9E8P7	Q9E8P7 beet soli-b
40	13	27.7	9	2	Q47410	Q47410 escherichia
41	13	27.7	9	4	Q9BYF9	Q9BYF9 homo sapien
42	13	27.7	9	4	Q9UGE4	Q9UGE4 homo sapien
43	13	27.7	9	6	Q9XSL0	Q9XSL0 capra hircu
44	13	27.7	9	8	P92072	P92072 euhadra her
45	12	25.5	7	12	Q65578	Q65578 bovine herp

#### ALIGNMENTS

#### RESULT 1

Q05403 ID Q05403 PRELIMINARY; PRT: 8 AA.  
AC Q05403;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE DNA for ORF.5 from chromosome XV (fragment).  
GN COQ3 AND YOL096C.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FY1679;  
RX MEDLINE=96021609; PubMed=8533473;  
RA Zumstein E., Pearson B.M., Kaloogeropoulos A., Schweizer M.;  
RT 'A 29.425 Kb segment on the left arm of yeast chromosome XV contains  
RL more than twice as many unknown as known open reading frames.';  
RL Yeast 11:975-986(1995).  
DR EMBL; X83121; CAA58183.1; .  
DR SGD; S0005456; COQ3.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 46.8%; Score 22; DB 3; Length 8;  
Best Local Similarity 80.0%; Pred. No. 6.7e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HSVK 8  
Db 3 HNVK 7

#### RESULT 2

P87488 ID P87488 PRELIMINARY; PRT: 8 AA.  
AC P87488;

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DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE Growth hormone 2 (Fragment).
GN GH-2-A OR GH-2-B.
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE OF 41-48 FROM N.A.
RX MEDLINE=94173883; PubMed=8127856;
RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
RT "One of two growth hormone genes in coho salmon is sex-linked.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1628-1631(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:0-0(0).
DR EMBL; U04930; AAD13472.1; -
DR EMBL; U04931; AAD13476.1; -
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 902 MW; 92233732D5A5B326 CRC64;

Query Match 38.3%; Score 18; DB 13; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHSVK 8
DB 2 KSVLK 7

RESULT 3
Q9UC36 PRELIMINARY; PRT; 9 AA.
AC Q9UC36;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinohara H., Goto S., Inaguna Y., Morishita R., Asano T.;
RT "Purification of small heat shock protein with alpha B crystallin
from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 38.3%; Score 18; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHS 5
DB 3 YPHS 6

RESULT 4
Q15894 PRELIMINARY; PRT; 8 AA.
AC Q15894;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE Cytochrome oxidase I (Fragment).

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (clone XP587B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32074; AAA73884.1; -
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 952 MW; EBC735B1E1F1B6D6 CRC64;

Query Match 36.2%; Score 17; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HSVV 7
DB 5 HSLV 8

RESULT 5
Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridoidea; Acrididae; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
restriction mapping and sequence of its ND-1(URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 36.2%; Score 17; DB 8; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYKH 4
DB 5 KLKH 8

RESULT 6
Q99182 PRELIMINARY; PRT; 7 AA.
AC Q99182;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).

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GN COI.  
 OS Gnatholebias zonatus.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Cyprinodontiformes; Aplocheilidae; Rivulidae; Gnatholebias.  
 OX NCBI\_TaxID=135316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20072928; PubMed=10603257;  
 RA Murphy W.J., Thomerson J.B., Collier G.E.;  
 RT "Phylogeny of the Neotropical killifish family Rivulidae  
 (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA  
 sequences.";  
 RL Mol. Phylogenet. Evol. 13:289-301(1999).  
 DR EMBL: AF002591; AAD01074.1; -  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;  
 Query Match 34.0%; Score 16; DB 8; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKH 4  
 Db 3 YQH 5  
 RESULT 7  
 Q9BYY5  
 ID Q9BY5 PRELIMINARY; PRT; 8 AA.  
 AC Q9BY5;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CAMP responsive element moderator (Fragment).  
 GN CREM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL: AY011664; AAG47575.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;  
 Query Match 34.0%; Score 16; DB 4; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YKHSV 6  
 Db 3 YCHKV 7  
 RESULT 8  
 Q9BFAO  
 ID Q9BFAO PRELIMINARY; PRT; 8 AA.  
 AC Q9BFAO;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CAMP responsive element moderator (Fragment).  
 GN CREM.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL: AY011664; AAG47575.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;  
 Query Match 34.0%; Score 16; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YKHSV 6  
 Db 3 YCHKV 7  
 RESULT 9  
 Q9BF99  
 ID Q9BF99 PRELIMINARY; PRT; 8 AA.  
 AC Q9BF99;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CAMP responsive element moderator (Fragment).  
 GN CREM.  
 OS Hylobates concolor (crested gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=29089;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL: AY011662; AAG47573.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;  
 Query Match 34.0%; Score 16; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YKHSV 6  
 Db 3 YCHKV 7  
 RESULT 10  
 Q28093  
 ID Q28093 PRELIMINARY; PRT; 9 AA.  
 AC Q28093;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Cytokeratin IV gene upstream region (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89231609; PubMed=2469572;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL: AY011661; AAG47572.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;  
 Query Match 34.0%; Score 16; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YKHSV 6  
 Db 3 YCHKV 7  
 RESULT 9  
 Q9BF99  
 ID Q9BF99 PRELIMINARY; PRT; 8 AA.  
 AC Q9BF99;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CAMP responsive element moderator (Fragment).  
 GN CREM.  
 OS Hylobates concolor (crested gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=29089;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL: AY011662; AAG47573.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;  
 Query Match 34.0%; Score 16; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 YKHSV 6  
 Db 3 YCHKV 7  
 RESULT 10  
 Q28093  
 ID Q28093 PRELIMINARY; PRT; 9 AA.  
 AC Q28093;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Cytokeratin IV gene upstream region (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89231609; PubMed=2469572;

RA Blessing M., Jorcano J.L., Franke W.W.;  
 RT "Enhancer elements directing cell-type-specific expression of  
 RT cyokeratin genes and changes of the epithelial cytoskeleton by  
 RT transfections of hybrid cyokeratin genes.";  
 RL EMBO J. 8:1117-126(1989).  
 DR EMBL; X14478; CAA32640.1; -.  
 KW Keratin.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1044 MW; 819A22D1B5B32B45 CRC64;

Query Match 34.0%; Score 16; DB 6; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YKHSV 6  
 | | |  
 DB 3 YKSTV 7

RESULT 11  
 Q99MG3 PRELIMINARY; PRT; 9 AA.  
 AC Q99MG3;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE NCAM protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MORE M.I., Kirsch F.P., Rathjen F.G.;  
 RT "Targeted ablation of NCAM and ankyrin-B results in disorganized lens  
 RT fibres leading to cataract formation.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF346472; AAK25814.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1039 MW; 32FCB721E3333327 CRC64;

Query Match 34.0%; Score 16; DB 11; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KYKH 4  
 | | |  
 DB 3 KKKH 6

RESULT 12  
 Q56429 PRELIMINARY; PRT; 8 AA.  
 AC Q56429;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GAPDH (Fragment).  
 OS Thermus thermophilus.  
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;  
 OC Thermaceae; Thermus.  
 OX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HB-8;  
 RX MEDLINE=89025722; PubMed=3052437;  
 RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;  
 RT "Nucleotide sequence of the phosphoglycerate kinase gene from the  
 RT extreme thermophile, Thermus thermophilus.";  
 RL Biochem. J. 254:509-517(1988).  
 DR EMBL; X12464; CAA31005.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 885 MW; 33C87333332C72B CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 VVKK 9  
 | | |  
 DB 3 VLKK 6

RESULT 13  
 Q95GNI PRELIMINARY; PRT; 9 AA.  
 AC Q95GNI;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein L36 (Fragment).  
 GN RPL36.  
 OS Pelargonium hortorum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Geraniales; Geraniaceae; Pelargonium.  
 OX NCBI\_TaxID=4031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21149877; PubMed=11251102;  
 RA Millen R.S., Olmstead R.G., Adams K.L., Palmer J.D., Lao N.T.,  
 RA Heggie L., Kavanagh T.A., Hibberd J.M., Gray J.C., Morden C.W.,  
 RA Calie P.J., Jermiin L.S., Wolfe K.H.;  
 RT "Many Parallel Losses of Infa from Chloroplast DNA during Angiosperm  
 RT Evolution with Multiple Independent Transfers to the Nucleus.";  
 RL Plant Cell 13:645-658(2001).  
 DR EMBL; AF347625; AAK38852.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1088 MW; 4B1D12D5BDC40053 CRC64;

Query Match 29.8%; Score 14; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 KYKHSVVK 8  
 | : | | |  
 DB 2 KIRASVRK 9

RESULT 14  
 O92766 PRELIMINARY; PRT; 9 AA.  
 AC O92766;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 OX NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DOG #5526/89;  
 RA Liermann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 RT proximal coding part of the F gene of wild-type and vaccine distemper  
 RT morbilliviruses.";  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026237; AAC09167.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1011 MW; F2B1732760533441 CRC64;

Query Match 29.8%; Score 14; DB 12; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 HSVVK 9  
 I: : I  
 Db 2 HNKIPK 7

## RESULT 15

Q9ILX6 PRELIMINARY; PRT; 9 AA.  
 AC Q9ILX6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE ORF 10-like protein (Fragment).  
 OS Macaca nemestrina rhadinovirus 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=123630;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MNE442N;  
 RX MEDLINE=20240083; PubMed=10775636;  
 RA Schultz E.R., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C.,  
 RA Rose T.M.;  
 RT "Characterization of two divergent lineages of macaque rhadinoviruses  
 RT related to Kaposi's sarcoma-associated herpesvirus.";  
 RL J. Virol. 74:4919-4928(2000).  
 DR EMBL; AF204167; AAF81665.1; -.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1003 MW; 41EBD5B7233AB2C7 CRC64;

Query Match 29.8%; Score 14; DB 12; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 6.7e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHSV 7  
 I: I I I I  
 Db 5 KLSVV 9

Search completed: January 29, 2003, 09:54:22  
 Job time : 29 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:46:43 ; Search time 34 Seconds  
(without alignments)  
35.272 Million cell updates/sec

Title: US-09-878-603-14  
Perfect score: 47  
Sequence: 1 KYKHSVVK 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 130868

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	22 AAB74059	Human C5a peptide
2	44	93.6	9	22 AAB74063	C-terminal truncat
3	43	91.5	9	22 AAB74064	C-terminal truncat
4	43	91.5	9	22 AAB74066	C-terminal truncat
5	39	83.0	9	22 AAB74065	C-terminal truncat
6	30	63.8	7	22 AAB82899	p53 common mutant
7	27	57.4	8	22 ABP16996	HIV B27 super moti
8	27	57.4	9	18 AAW43875	Specific human leu
9	27	57.4	9	21 AAY95886	Human MHC class I
10	27	57.4	9	22 ABP14323	HIV A03 super moti

11	27	57.4	9	22 ABP15261	HIV A24 super moti
12	27	57.4	9	22 ABP20218	HIV A03 motif env
13	27	57.4	9	22 ABP22540	HIV A11 motif env
14	27	57.4	9	22 ABP24101	HIV A24 motif env
15	25	53.2	6	22 AAB82900	p53 common mutant
16	25	53.2	8	22 AAB30993	Peptide derived fr
17	25	53.2	8	22 AAB31074	Polyepitopic pepti
18	25	53.2	8	22 AAB31100	A polyepitopic fra
19	25	53.2	9	17 AAR97537	Antigenic peptide
20	25	53.2	9	20 AAY53377	p53 epitope (aa 21
21	25	53.2	9	20 AAY40200	Amino acid sequenc
22	25	53.2	9	20 AAY26716	HLA-B8 binding p53
23	25	53.2	9	22 AAG89419	p53 DR supermotif
24	25	53.2	9	22 AAB30994	Peptide derived fr
25	25	53.2	9	22 AAB31075	Polyepitopic pepti
26	25	53.2	9	22 AAB31101	A polyepitopic fra
27	24	51.1	9	14 AAR41610	TRIP-23. Syntheti
28	24	51.1	9	14 AAR41621	TRIP-40. Syntheti
29	24	51.1	9	19 AAW59307	Non-pollo enterovi
30	24	51.1	9	23 ABB94713	CTL epitope HLA pe
31	24	51.1	9	23 ABB94713	CTL epitope HLA pe
32	23	48.9	6	20 AAW91028	Peptide inhibiting
33	23	48.9	6	21 AAB27341	Beta-catenin deriv
34	23	48.9	6	23 AAG69114	Randomised ligand
35	23	48.9	7	20 AAW91026	Peptide inhibiting
36	23	48.9	7	21 AAB27339	Beta-catenin deriv
37	23	48.9	8	22 ABP16995	HIV B27 super moti
38	23	48.9	9	22 ABP15360	HIV A24 super moti
39	23	48.9	9	22 ABP24052	HIV A24 motif env
40	22	46.8	5	16 AAR85139	Mutant p53 epitope
41	22	46.8	5	20 AAW91000	Peptide inhibiting
42	22	46.8	5	21 AAB27284	Beta-catenin deriv
43	22	46.8	6	17 AAR90580	TRAF1 peptide. Mu
44	22	46.8	6	20 AAW91036	Peptide inhibiting
45	22	46.8	6	20 AAW91027	Peptide inhibiting

#### ALIGNMENTS

RESULT 1  
AAB74059  
ID AAB74059 standard; Peptide; 9 AA.  
XX  
AC AAB74059;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE Human C5a peptide fragment #4.  
XX  
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;  
KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
KW wound; anaphylatoxin; sepsis.  
XX  
OS Homo sapiens.  
XX  
PN WO200115731-A1.  
XX  
PD 08-MAR-2001.  
XX  
PF 31-AUG-2000; 2000WO-US24219.  
XX  
PR 31-AUG-1999; 99US-0387671.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Ward PA, Huber-Lang M, Sarma V;  
XX  
DR WPI; 2001-226665/23.  
XX  
DR N-PSDB; AAF75796.  
XX  
PT Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a





KW C5a; complement; antibody; bacterial infection; sinusitis;  
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KW wound; anaphylatoxin; sepsis.

OS Unidentified.

XX WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMI ) UNIV MICHIGAN.

PI Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure; Page 29; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

XX Sequence 9 AA;

Query Match 91.5%; Score 43; DB 22; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9

||||| ||

DB 1 KYKHSVAKK 9

RESULT 5

AAB74065

ID AAB74065 standard; Peptide; 9 AA.

XX AC AAB74065;

XX DT 16-MAY-2001 (first entry)

XX C-terminal truncated C5a peptide #3.

XX C5a; complement; antibody; bacterial infection; sinusitis;  
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
 KW wound; anaphylatoxin; sepsis.

OS Unidentified.

XX WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMI ) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX

DR WPI; 2001-226665/23.

XX

PT Compositions for treating blood-borne and toxin mediated diseases and  
 PT treatment of sepsis in humans and other animals comprises anti-C5a  
 PT antibodies generated against C-terminal truncated C5a peptides -

XX

Disclosure; Page 29; 84pp; English.

XX

CC The present sequence is a C-terminal truncated C5a peptide fragment. The  
 CC present invention relates to an antibody specific for the present  
 CC sequence. The C5a-antibody can be used in a therapeutic composition,  
 CC which is useful for treating a subject suffering from bacterial  
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or  
 CC urinary tract infections or infections in wounds. In addition, the C5a  
 CC antibody can be used for treating sepsis. C5a is also known as  
 CC anaphylatoxin.

XX Sequence 9 AA;

Query Match 83.0%; Score 39; DB 22; Length 9;

Best Local Similarity 77.8%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9

||||| ||

DB 1 KYKHSAAKK 9

RESULT 6

AAB82899

ID AAB82899 standard; Peptide; 7 AA.

XX AC AAB82899;

XX DT 26-NOV-2001 (first entry)

XX p53 common mutant antigen.

XX Single chain antibody; ME1; p53; common mutant epitope; human;

KW tumour suppressor protein; therapy; cancer.

XX

OS Homo sapiens.

OS Synthetic.

PN WO200168801-A2.

XX PD 20-SEP-2001.

XX PF 09-MAR-2001; 2001WO-IL00225.

XX PR 16-MAR-2000; 2000US-0526738.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX Solomon B, Cohen G, Govorko D;

XX WPI; 2001-590047/66.

PT Novel single chain antibody molecule specifically recognizing common  
 PT mutant epitope in mutant p53 but not in wild-type p53, and  
 PT polynucleotides encoding antibodies, useful for preparing medicament  
 PT for treating cancer -

XX Disclosure; Page 13; 46pp; English.

XX The present sequence is that of the common mutant epitope of  
 CC mutant p53 protein. The epitope is exposed on mutant p53 but  
 CC not on wild-type p53. In the present case, an additional Lys  
 CC amino acid residue has been added to the N-terminal end of the  
 CC native epitope in order to facilitate covalent coupling to  
 CC microtiter plates. The invention provides a single chain antibody  
 CC (scFv), designated ME1 (see AAB82897), which specifically

CC recognises the common mutant epitope in mutant p53 protein but not in wild-type p53. ME1, DNA encoding it and a vector comprising the DNA, are used in claimed methods for treating a patient suffering from a disease related to mutation of the p53 gene, especially cancer.

XX  
SQ Sequence 7 AA; Query Match 63.8%; Score 30; DB 22; Length 7; Best Local Similarity 71.4%; Pred. No. 7.8e+05; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKHSVV 7  
Db 1 KFRHSVV 7  
:::|||||

RESULT 7  
ABP16996  
ID ABP16996 standard; Peptide; 8 AA.  
XX  
AC ABP16996;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV B27 super motif env peptide #21.  
XX  
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US27766.  
XX  
PR 05-OCT-1999; 99US-0412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Grey HM;  
XX  
DR WPI: 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -  
XX  
PS Claim 32; Page 217; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412

CC represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA;

Query Match 57.4%; Score 27; DB 22; Length 8;  
Best Local Similarity 71.4%; Pred. No. 7.8e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8  
II: |||

Db 1 YKYKVVK 7  
II: |||

RESULT 8

AAW43875  
ID AAW43875 standard; peptide; 9 AA.

XX  
AC AAW43875;

XX  
DT 20-APR-1998 (first entry)

XX  
DE Specific human leukocyte antigen binding peptide #79.

XX  
KW Human leukocyte antigen; HLA; vaccine; bacterial infection; viral;  
KW cytotoxic T-cell; CTL; immunogenic peptide; cancer.

XX  
OS Synthetic.

XX  
OS Human immunodeficiency virus type 1.

XX  
PN WO9734617-A1.

XX  
PD 25-SEP-1997.

XX  
PF 21-MAR-1997; 97WO-US04451.

XX  
PR 20-MAR-1997; 97US-0821739.

XX  
PR 21-MAR-1996; 96US-0013833.

XX  
PA (CYTE-) CYTEL CORP.

XX  
PI Celis E, Grey HM, Kubo RT, Sette A;

XX  
DR WPI: 1997-489250/45.

XX  
PT Specific human leukocyte antigen binding peptide - used in vaccines for the treatment and prevention of e.g. bacterial or viral infection and cancer

XX  
PS Claim 19; Page 39; 49pp; English.

XX The present sequence represents a specific example of an immunogenic peptide which was used in a new method of inducing a cytotoxic T cell (CTL) response against a preselected antigen in a patient. The method comprises contacting CTLs from the patient with the immunogenic peptide (containing defined motifs) which binds one of the four HLA MHC products (HLA-A\*2, HLA-A1, HLA-A11 or HLA-A24.1, the peptide having a dissociation constant (Kd) of less than 5 x 10<sup>-7</sup> M. Immunogens are viral, e.g. human immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and hepatitis C virus (HCV) or cancer antigens and are used in vaccines for the prevention and treatment of viral infection and cancer. The immunogens may be administered to the patient as a nucleic acid encoding the peptide (gene vaccine).

XX  
SQ Sequence 9 AA;

Query Match 57.4%; Score 27; DB 18; Length 9;  
Best Local Similarity 71.4%; Pred. No. 7.8e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8  
II: |||

Db 2 YKYKVVK 8  
II: |||

RESULT 9  
 AAY95886  
 ID AAY95886 standard; Peptide: 9 AA.  
 XX  
 AC AAY95886;  
 XX  
 DT 20-NOV-2000 (first entry)  
 XX  
 DE Human MHC class I allele HLA-A0201 binding motif CLP-505.  
 XX  
 KW Major histocompatibility complex class I; MHC class I; human;  
 KW HLA-A0201; HIV-1; Human immunodeficiency virus type 1; gp140;  
 KW immunogen; DNA vaccine.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 FN WO200050604-A1.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 24-FEB-2000; 2000WO-CA00190.  
 XX  
 PR 24-FEB-1999; 99US-0256194.  
 XX  
 PA (CONN-) CONNAUGHT LAB LTD.  
 XX  
 PI Sia CDY, Cao S, Persson R, Rovinski B, Parrington M;  
 XX  
 DR WPI; 2000-565457/52.  
 XX  
 PT Vectors comprising sequences encoding the extracellular fragment of  
 PT gp140 of a primary human immunodeficiency virus (HIV)-1 isolate, useful  
 PT for vaccinating against HIV-1 -  
 XX  
 PS Claim 16; Page 18; 37pp; English.  
 XX  
 CC The present sequence is that of CLP-505, a major histocompatibility  
 CC complex (MHC) class-I restricted motif of the extracellular envelope  
 CC fragment, gp140 (see AAY95882), of HIV-1 isolate BX08. The invention  
 CC provides vectors comprising sequences encoding gp140, useful for  
 CC vaccinating against HIV-1. The gp140 protein is rich in motifs  
 CC restricted to both the human and murine MHC class I alleles (see  
 CC AAY95883-94). The present peptide is HLA-A0201 restricted.  
 CC Immunisation with an immunogen expressing the gp140 protein leads  
 CC to the generation of peptides with class I binding capability to  
 CC allow the induction of HIV-1-specific cytotoxic T lymphocytes  
 CC capable of killing virus-infected cells to limit infection.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.4%; Score 27; DB 21; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 YKHSVVK 8  
 ||: |||  
 Db 2 YKRVVK 8  
 RESULT 10  
 ABP14323  
 ID ABP14323 standard; Peptide: 9 AA.  
 XX  
 AC ABP14323;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A03 super motif env peptide #63.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; Immune response; epitope;  
 KW

KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 162; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC AP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.4%; Score 27; DB 22; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 YKHSVVK 8  
 ||: |||  
 Db 3 YKRVVK 9  
 RESULT 11  
 ABP15261  
 ID ABP15261 standard; Peptide: 9 AA.  
 XX  
 AC ABP15261;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A24 super motif env peptide #141.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; Immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.

```

XX PN WO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX XX
XX PF 05-OCT-2000; 2000WO-US27766.
XX XX
XX PR 05-OCT-1999; 99US-0412863.
XX XX
XX PR 05-OCT-1999; 99US-0412863.
XX XX
XX PA (EPIM-) EPIMUNE INC.
XX XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX XX
XX DR WPI; 2001-354887/37.
XX XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1.
XX XX
XX PS Claim 32; Page 181; 448pp; English.
XX XX
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX XX
XX SQ Sequence 9 AA;
XX
XX Query Match 57.4%; Score 27; DB 22; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 YKHSVVK 8
XX ||: |||
XX Db 2 YKRVVK 8
XX
XX RESULT 12
XX ABP20218
XX ID ABP20218 standard; Peptide: 9 AA.
XX XX
XX AC ABP20218;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DE HIV A03 motif env peptide #422.
XX XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX XX
XX OS Human immunodeficiency virus type 1.
XX XX
XX PN WO200124810-A1.
XX PF

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```

PD XX 12-APR-2001.
PF XX
XX PF 05-OCT-2000; 2000WO-US27766.
XX XX
XX PR 05-OCT-1999; 99US-0412863.
XX XX
XX PA (EPIM-) EPIMUNE INC.
XX XX
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX XX
XX DR WPI; 2001-354887/37.
XX XX
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1.
XX XX
XX PS Claim 32; Page 284; 448pp; English.
XX XX
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX XX
XX SQ Sequence 9 AA;
XX
XX Query Match 57.4%; Score 27; DB 22; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2 YKHSVVK 8
XX ||: |||
XX Db 3 YKRVVK 9
XX
XX RESULT 13
XX ABP22540
XX ID ABP22540 standard; Peptide: 9 AA.
XX XX
XX AC ABP22540;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DE HIV A11 motif env peptide #263.
XX XX
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX XX
XX OS Human immunodeficiency virus type 1.
XX XX
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX XX
XX PF 05-OCT-2000; 2000WO-US27766.

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XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX XX WPI; 2001-354887/37.
XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1.
XX PS Claim 32; Page 331; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABP25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA;

Query Match 57.4%; Score 27; DB 22; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8
DB 3 YKYKVK 9

RESULT 14
ABP24101
ID ABP24101 standard; Peptide; 9 AA.
XX AC
XX AC ABP24101;
XX DT 15-JUL-2002 (first entry)
XX DE HIV A24 motif env peptide #67.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX OS
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX XX
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PI
XX XX

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PA (EPIM-) EPIMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX XX WPI; 2001-354887/37.
XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1.
XX PS Claim 32; Page 363; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABP25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP11501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA;

Query Match 57.4%; Score 27; DB 22; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8
DB 2 YKYKVK 8

RESULT 15
AAB82900
ID AAB82900 standard; Peptide; 6 AA.
XX AC
XX AC AAB82900;
XX DT 26-NOV-2001 (first entry)
XX DE p53 common mutant antigen.
XX KW Single chain antibody; ME1; p53; common mutant epitope; human;
XX KW therapy; cancer.
XX OS Homo sapiens.
XX XX
XX PN WO200168801-A2.
XX PD 20-SEP-2001.
XX XX
XX PF 09-MAR-2001; 2001WO-IL00225.
XX XX
XX PR 16-MAR-2000; 2000US-0526738.
XX XX
XX PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX PI Solomon B, Cohen G, Govorko D;
XX XX

```

DR WPI; 2001-590047/66.  
 XX  
 PT Novel single chain antibody molecule specifically recognizing common  
 PT mutant epitope in mutant p53 but not in wild-type p53, and  
 PT polynucleotides encoding antibodies, useful for preparing medicament  
 PT for treating cancer  
 XX  
 PS Disclosure; Page 6; 46pp; English.  
 XX  
 CC The present sequence is that of the common mutant epitope of  
 CC mutant p53 protein. The epitope is exposed on mutant p53 but  
 CC not on wild-type p53. The invention provides a single chain  
 CC antibody (scFv), designated ME1 (see A882897), which specifically  
 CC recognises the common mutant epitope in mutant p53 protein but not  
 CC in wild-type p53. ME1, DNA encoding it and a vector comprising the  
 CC DNA, are used in claimed methods for treating a patient suffering  
 CC from a disease related to mutation of the p53 gene, especially  
 CC cancer.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 53.2%; Score 25; DB 22; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKHSVV 7  
 Db 1 FRHSVV 6

Search completed: January 29, 2003, 09:53:29  
 Job time : 35 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 09:54:29 ; Search time 11 seconds  
(without alignments)  
16.510 Million cell updates/sec

Title: US-09-878-603-14

Perfect score: 47

Sequence: 1 KYKHSVVKK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 19373

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 13: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	47	100.0	9	US-09-878-603-14	Sequence 14, Appl
2	44	93.6	9	US-09-878-603-20	Sequence 20, Appl
3	43	91.5	9	US-09-878-603-21	Sequence 21, Appl
4	43	91.5	9	US-09-878-603-23	Sequence 23, Appl
5	39	83.0	9	US-09-878-603-22	Sequence 22, Appl
6	27	57.4	8	US-09-243-079-29	Sequence 29, Appl
7	27	57.4	8	US-09-243-079-30	Sequence 30, Appl
8	27	57.4	9	US-08-821-739A-79	Sequence 79, Appl
9	24	51.1	8	US-09-984-056-69	Sequence 69, Appl
10	24	51.1	8	US-09-984-057-69	Sequence 69, Appl
11	22	46.8	8	US-09-243-079-28	Sequence 28, Appl
12	22	46.8	9	US-09-753-831-33	Sequence 33, Appl
13	21	44.7	7	US-09-996-288-69	Sequence 69, Appl
14	21	44.7	7	US-09-796-848A-21	Sequence 21, Appl
15	21	44.7	7	US-09-832-723-64	Sequence 64, Appl
16	21	44.7	8	US-10-012-035A-14	Sequence 14, Appl
17	21	44.7	8	US-09-735-274-14	Sequence 14, Appl
18	21	44.7	9	US-10-012-035A-13	Sequence 13, Appl
19	21	44.7	9	US-09-735-274-13	Sequence 13, Appl

20	21	44.7	9	10	US-09-834-765-45	Sequence 45, Appl
21	21	44.7	9	10	US-09-834-765-55	Sequence 55, Appl
22	20	42.6	7	10	US-09-898-461-10	Sequence 10, Appl
23	20	42.6	8	10	US-09-243-079-31	Sequence 31, Appl
24	20	42.6	9	9	US-09-769-145-71	Sequence 71, Appl
25	20	42.6	9	9	US-09-769-145-72	Sequence 72, Appl
26	20	42.6	9	9	US-09-909-460-93	Sequence 93, Appl
27	20	42.6	9	12	US-10-006-982-29	Sequence 29, Appl
28	20	42.6	9	12	US-10-006-982-31	Sequence 31, Appl
29	20	42.6	9	12	US-10-006-982-32	Sequence 32, Appl
30	19	40.4	6	10	US-09-808-387-43	Sequence 43, Appl
31	19	40.4	8	9	US-10-136-734-14	Sequence 14, Appl
32	19	40.4	9	10	US-09-918-243-32	Sequence 32, Appl
33	19	40.4	9	10	US-09-918-243-79	Sequence 79, Appl
34	19	40.4	9	10	US-09-918-243-87	Sequence 87, Appl
35	19	40.4	9	10	US-09-918-243-110	Sequence 110, Appl
36	19	40.4	9	10	US-09-905-083-32	Sequence 32, Appl
37	19	40.4	9	10	US-09-905-083-79	Sequence 79, Appl
38	19	40.4	9	10	US-09-905-083-87	Sequence 87, Appl
39	19	40.4	9	10	US-09-905-083-110	Sequence 110, Appl
40	18	38.3	5	9	US-09-769-145-12	Sequence 12, Appl
41	18	38.3	5	9	US-09-769-145-16	Sequence 16, Appl
42	18	38.3	5	10	US-09-804-682-167	Sequence 167, Appl
43	18	38.3	5	10	US-09-234-395-309	Sequence 309, Appl
44	18	38.3	5	10	US-09-234-395-311	Sequence 311, Appl
45	18	38.3	5	10	US-09-305-928-309	Sequence 309, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-878-603-14  
; Sequence 14, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czermak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: UM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-878-603-14

Query Match 100.0%; Score 47; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred No. 1e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9

Db 1 KYKHSVVKK 9

##### RESULT 2

US-09-878-603-20  
; Sequence 20, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czermak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis

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; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-20

Query Match          93.6%; Score 44; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. le+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9
Db 1 KYKHTYVKK 9

RESULT 3
US-09-878-603-21
; Sequence 21, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-21

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Best Local Similarity 88.9%; Pred. No. le+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9
Db 1 KYKHSVVKK 9

RESULT 4
US-09-878-603-23
; Sequence 23, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
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; NUMBER OF SEQ ID NOS: 74
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-23

Query Match          91.5%; Score 43; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. le+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYKHSVVKK 9
Db 1 KYKHSVVKK 9

RESULT 5
US-09-878-603-22
; Sequence 22, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-22

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Best Local Similarity 77.8%; Pred. No. le+05;
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QY 1 KYKHSVVKK 9
Db 1 KYKHSAAKK 9

RESULT 6
US-09-243-079-29
; Sequence 29, Application US/09243079
; Patent No. US20020081566A1
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY
; FILE REFERENCE: 29928-PCT-USA-1
; CURRENT APPLICATION NUMBER: US/09/243,079
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 08/335,733
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: PCT/IT93/00049
; PRIOR FILING DATE: 1993-05-10
; PRIOR APPLICATION NUMBER: RM92A/000350
; PRIOR FILING DATE: 1992-05-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-243-079-29

Query Match          57.4%; Score 27; DB 10; Length 8;
Best Local Similarity 71.4%; Pred. No. 1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8
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Db 2 YKYKVK 8

RESULT 7
US-09-243-079-30
; Sequence 30, Application US/09243079
; Patent No. US20020081566A1
; GENERAL INFORMATION:
; APPLICANT: Beretta, Alberto
; TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY
; FILE OF INVENTION: HOMOLOGOUS TO HLA
; FILE REFERENCE: 29928-PCT-USA-1
; CURRENT APPLICATION NUMBER: US/09/243,079
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: 08/335,733
; PRIOR FILING DATE: 1994-11-10
; PRIOR APPLICATION NUMBER: PCT/IT93/00049
; PRIOR FILING DATE: 1993-05-10
; PRIOR APPLICATION NUMBER: RM92A/000350
; PRIOR FILING DATE: 1992-05-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-243-079-30

Query Match          57.4%; Score 27; DB 10; Length 8;
Best Local Similarity 71.4%; Pred. No. 1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8
   ||: |||
Db 1 YKYKVK 7

RESULT 8
US-08-821-739A-79
; Sequence 79, Application US/08821739A
; Patent No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-03-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-79

Query Match          57.4%; Score 27; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVVK 8
   ||: |||
Db 2 YKYKVK 8

RESULT 9
US-09-984-056-69
; Sequence 69, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 69
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-056-69

Query Match          51.1%; Score 24; DB 10; Length 8;
Best Local Similarity 62.5%; Pred. No. 1e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYKHSVVK E
   ||: |||
Db 1 KKRHTVVK E

RESULT 10
US-09-984-057-69
; Sequence 69, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
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; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 69  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-984-057-69

Query Match 51.1%; Score 24; DB 10; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYKHSVVK 8  
| | | | |  
DB 1 KKKHTVKK 8

RESULT 11  
US-09-243-079-28  
; Sequence 28, Application US/09243079  
; Patent No. US20020081566A1  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY  
; FILE OF INVENTION: HOMOLOGOUS TO HLA  
; FILE REFERENCE: 29928-PCT-USA-I  
; CURRENT APPLICATION NUMBER: US/09/243,079  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 08/335,733  
; PRIOR FILING DATE: 1994-11-10  
; PRIOR APPLICATION NUMBER: PCT/IT93/00049  
; PRIOR FILING DATE: 1993-05-10  
; PRIOR APPLICATION NUMBER: RM92A/000350  
; PRIOR FILING DATE: 1992-05-11  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
US-09-243-079-28

Query Match 46.8%; Score 22; DB 10; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVV 7  
| | | | |  
DB 3 YKVKV 8

RESULT 12  
US-09-753-831-33  
; Sequence 33, Application US/09753831  
; Patent No. US20020137683A1  
; GENERAL INFORMATION:  
; APPLICANT: Hogan, Kevin T.  
; APPLICANT: Ross, Mark M.  
; TITLE OF INVENTION: C-SKI Oncogene-Derived Peptides for Prevention,  
; FILE OF INVENTION: Treatment and Diagnosis of Cancer  
; FILE REFERENCE: 26747-27  
; CURRENT APPLICATION NUMBER: US/09/753,831  
; CURRENT FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: U.S. 60/174296  
; PRIOR FILING DATE: 2000-01-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:No. US20020137683A1aleptide  
; OTHER INFORMATION: derived from the human C-SKI oncoprotein.  
US-09-753-831-33

Query Match 46.8%; Score 22; DB 10; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKHSVVK 8  
| | | | |  
DB 1 FLHEVVK 7

RESULT 13  
US-09-996-288-69  
; Sequence 69, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophyl  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-69

Query Match 44.7%; Score 21; DB 9; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKHS 5  
| | | | |  
DB 3 YRHS 6

RESULT 14  
US-09-796-848A-21  
; Sequence 21, Application US/09796848A  
; Patent No. US20020098189A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James F.  
; APPLICANT: Johnson, Leslie S.  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.

; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of  
; TITLE OF INVENTION: Producing Them  
; FILE REFERENCE: 463201-526  
; CURRENT APPLICATION NUMBER: US/09/796,848A  
; CURRENT FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 0.S. 60/186,252  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:High potency
; OTHER INFORMATION: CDR sequence.
US-09-796-848A-21

Query Match      44.7%; Score 21; DB 10; Length 7;
Best Local Similarity 75.0%; Pred.No.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKHS 5
Db 3 YRHS 6

RESULT 15
US-09-832-723-64
; Sequence 64, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-64

Query Match      44.7%; Score 21; DB 10; Length 7;
Best Local Similarity 60.0%; Pred.No.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSV 6
Db 3 YKHDL 7
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Search completed: January 29, 2003, 09:58:05  
Job time : 11 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 09:52:55 ; Search time 14 Seconds  
(without alignments)  
18.915 Million cell updates/sec

Title: US-09-878-603-14

Perfect score: 47

Sequence: 1 KYKHSVYKK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 66399

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A-COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS-COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	57.4	8	3	US-08-335-733D-29
2	27	57.4	8	3	US-08-335-733D-30
3	27	57.4	9	4	US-09-256-194-6
4	25	53.2	9	5	PCT-US95-16415-30
5	22	46.8	6	1	US-08-331-394-42
6	22	46.8	6	1	US-08-250-858-42
7	22	46.8	6	1	US-08-446-915-42
8	22	46.8	6	2	US-08-744-139-42
9	22	46.8	6	5	PCT-US95-06639-42
10	22	46.8	8	1	US-08-594-447-29
11	22	46.8	8	1	US-08-541-964-28
12	22	46.8	8	3	US-08-665-647-43
13	22	46.8	8	3	US-08-335-733D-28
14	22	46.8	9	3	US-08-159-339A-621
15	21	44.7	4	3	US-08-654-623-62
16	21	44.7	5	4	US-08-751-344B-29
17	21	44.7	7	2	US-08-188-583-42
18	21	44.7	7	4	US-08-026-143B-49
19	21	44.7	7	5	PCT-US92-10621-49
20	21	44.7	7	5	PCT-US94-02233-49
21	21	44.7	8	2	US-08-188-583-52
22	21	44.7	9	1	US-08-146-152-3
23	20	42.6	4	3	US-08-654-623-66
24	20	42.6	6	1	US-08-406-192-41
25	20	42.6	6	2	US-08-545-151-41
26	20	42.6	6	4	US-08-635-928-12
27	20	42.6	6	5	PCT-US93-01669-25

28	20	42.6	8	2	US-08-147-777-4	Sequence 4, Appl
29	20	42.6	8	3	US-08-335-733D-31	Sequence 31, Appl
30	20	42.6	8	3	US-08-452-872-4	Sequence 4, Appl
31	20	42.6	8	3	US-08-582-776C-28	Sequence 28, Appl
32	20	42.6	8	3	US-08-434-831B-28	Sequence 28, Appl
33	20	42.6	8	4	US-08-845-541B-31	Sequence 31, Appl
34	20	42.6	8	5	PCT-US93-03985-4	Sequence 4, Appl
35	20	42.6	9	1	US-08-787-547-93	Sequence 93, Appl
36	20	42.6	9	2	US-08-318-856A-14	Sequence 14, Appl
37	20	42.6	9	3	US-08-893-534A-29	Sequence 29, Appl
38	20	42.6	9	3	US-08-893-534A-32	Sequence 31, Appl
39	20	42.6	9	3	US-08-893-534A-32	Sequence 32, Appl
40	20	42.6	9	3	US-08-159-339A-1187	Sequence 1187, Ap
41	20	42.6	9	4	US-08-996-679-29	Sequence 29, Appl
42	20	42.6	9	4	US-08-996-679-31	Sequence 31, Appl
43	20	42.6	9	4	US-08-996-679-32	Sequence 32, Appl
44	20	42.6	9	4	US-09-115-395-47	Sequence 47, Appl
45	20	42.6	9	4	US-09-115-395-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1  
US-08-335-733D-29  
; Sequence 29, Application US/08335733D  
; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,733D  
; FILING DATE: 10-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacLeod, Janet M  
; REGISTRATION NUMBER: 35,263  
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2500  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-335-733D-29

Query Match 57.4% Score 27; DB 3; Length 8;

Best Local Similarity 71.4%; Pred. No. 2e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0;  
Gaps 0;

QY 2 YKHSVVK 8  
||: |||

Dd 2 YKYKVVK 8

RESULT 2  
US-08-335-733D-30  
; Sequence 30, Application US/08335733D  
; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.

Query Match 57.4%; Score 27; DB 3; Length 8;  
Best Local Similarity 71.4%; Pred. No. 2e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	2	YKHSVVK	8
		:	
Db	1	YKYKVVK	7

RESULT 3  
US-09-256-194-6  
; Sequence 6, Application US/09256194  
; Patent No. 6395714  
; GENERAL INFORMATION:  
; APPLICANT: Sia, Charles D.Y.  
; APPLICANT: Cao, Shi Xian

```

; APPLICANT: Persson, Roy
; APPLICANT: Rovinski, Benjamin
; TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV-1 ISOLATE
; FILE REFERENCE: 1038-920
; CURRENT APPLICATION NUMBER: US/09/256,194
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus type 1
; US-09-256-194-6

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Query Match 57.4%; Score 27; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. NO. 2e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YKHSVVK E  
||: |||  
Db 2 YKYKVVK 8

```

RESULT 4
PCT-US95-16415-30
; Sequence 30, Application PC/TUS95S16415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16415
; FILING DATE: 13-DEC-1995
; CLASSIFICATION:

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Query Match 53.2%; Score 25; DB 5; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels

QY . 2 YKHSV 7  
Db 3 FRHSV 8

```

RESULT 5
US-08-331-394-42
; Sequence 42, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-331-394-42

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```

Query Match 46.8%; Score 22; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 3 KHSVVK 8
Db 1 KHAYVK 6

```

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RESULT 6
US-08-250-858-42
; Sequence 42, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-250-858-42

```

```

Query Match 46.8%; Score 22; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 KHSVVK 8
Db 1 KHAYVK 6

```

```

RESULT 7
US-08-446-915-42
; Sequence 42, Application US/08446915
; Patent No. 5741657
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-446-915-42
Query Match 46.8%; Score 22; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHSVVK 8
Db 1 KHAYVK 6

RESULT 8
US-08-744-139-42
; Sequence 42, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; NAME: Dreger, Ginger R.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-744-139-42
Query Match 46.8%; Score 22; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHSVVK 8
Db 1 KHAYVK 6

RESULT 9
PCT-US95-06639-42
; Sequence 42, Application PC/TUS9506639
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; NAME: Dreger, Ginger R.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2PCT
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-06639-42
Query Match 46.8%; Score 22; DB 5; Length 6;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KHSVVK 8
Db 1 KHAYVK 6

RESULT 10
US-08-594-447-29
; Sequence 29, Application US/08594447
; Patent No. 5776716
; GENERAL INFORMATION:
; APPLICANT: Ron, Dorit
; APPLICANT: Napolitano, Eugene W.
; APPLICANT: Voronova, Anna F.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES THEREOF
; TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1838
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,447
```

;; FILING DATE: 31-JAN-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Murashige, Kate H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 22550-20025.24  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 822-0168  
;; TELEX: 90-4030 MRSNFOERSWSH  
;; INFORMATION FOR SEQ ID NO: 29:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..8  
;; OTHER INFORMATION: /label= nu-VI-6  
US-08-594-447-29

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSVVKK 9  
||: ||  
Db 1 HSLFKK 6

RESULT 11  
US-08-541-964-28  
; Sequence 28, Application US/08541964  
; Patent No. 5783405  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; APPLICANT: Kauvar, Lawrence M.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS  
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,964  
; FILING DATE: 10-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.23  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; NAME/KEY: Peptide  
;; LOCATION: 1..8  
;; OTHER INFORMATION: /label= nu-VI-6  
US-08-541-964-28

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSVVKK 9  
||: ||  
Db 1 HSLFKK 6

RESULT 12  
US-08-665-647-43  
; Sequence 43, Application US/08665647  
; Patent No. 5935803  
; GENERAL INFORMATION:  
; APPLICANT: Dasquez, Nicki J.  
; APPLICANT: Ron, Dorit  
; APPLICANT: Voronova, Anna F.  
; APPLICANT: Napolitano, Eugene W.  
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS  
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW - Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,647  
; FILING DATE: 18-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22550-20025.25  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 822-0168  
; TELEX: 90-4030 MRSNFOERSWSH  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..8  
; OTHER INFORMATION: /label= nu-VI-6  
US-08-665-647-43

Query Match 46.8%; Score 22; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSVVKK 9  
||: ||  
Db 1 HSLFKK 6



RESULT 13  
US-08-335-733D-28  
; Sequence 28, Application US/08335733D  
; Patent No. 6042831  
; GENERAL INFORMATION:  
; APPLICANT: Beretta, Alberto  
; TITLE OF INVENTION: HIV PROTEIN EPITOPES,  
; TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P.  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,733D  
; FILING DATE: 10-NOV-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacLeod, Janet M  
; REGISTRATION NUMBER: 35,263  
; REFERENCE/DOCKET NUMBER: A29928-PCT-USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-408-2500  
; TELEFAX: 212-765-2519  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-335-733D-28

Query Match 46.8%; Score 22; DB 3; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKHSVV 7  
|||  
Db 3 YKQVV 8

RESULT 14  
US-08-159-339A-621  
; Sequence 621, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/936,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-0050300S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 621:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-159-339A-621

Query Match 46.8%; Score 22; DB 3; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKHSVV 7  
|||  
Db 3 YKHEQV 8

RESULT 15  
US-08-654-623-62  
; Sequence 62, Application US/08654623  
; Patent No. 6010884  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, Andrew D  
; APPLICANT: Holliger, Kaspar-Philipp  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Fisch, Igor  
; APPLICANT: Winter, Gregory P  
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/654,623

;; FILING DATE: 29-MAY-1996  
;; CLASSIFICATION: 435  
;; PRIORITY APPLICATION: (C12N 1/21, C12R 1:19)  
;; APPLICATION NUMBER: GB 9225453.1  
;; FILING DATE: 04-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9300816.7  
;; FILING DATE: 16-JAN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93303614.7  
;; FILING DATE: 10-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9319969.3  
;; FILING DATE: 22-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/GB93/02492  
;; FILING DATE: 03-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9412147.2  
;; FILING DATE: 17-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/GB94/02662  
;; FILING DATE: 05-DEC-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/448,418  
;; FILING DATE: 02-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: David W. Clough  
;; REGISTRATION NUMBER: 36,107  
;; REFERENCE/DOCKET NUMBER: 28111/33259  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312) 474-6300  
;; INFORMATION FOR SEQ ID NO: 62:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-654-623-62

Query Match 44.7%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KHSV 6  
Db 1 KHSV 4

Search completed: January 29, 2003, 09:55:04  
Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 09:57:54 ; Search time 15 Seconds  
(without alignments)  
38.454 Million cell updates

Title: US-09-878-603-15  
Perfect score: 32  
Sequence: 1 VNND 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

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Minimum DB seq length: 0
Maximum DB seq length: 6
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 s
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Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	17	53.1	5	2	A32014		tram protein - Esc
2	13	40.6	5	2	PT0656		T-cell receptor be
3	13	40.6	6	2	PT0510		T-cell receptor be
4	13	40.6	6	2	PT0599		T-cell receptor be
5	13	40.6	6	2	S29881		Na+/K+-exchanging
6	12	37.5	5	2	PT0573		T-cell receptor be
7	12	37.5	6	2	PC4127		hypothetical 6 pro
8	12	37.5	6	2	PT0650		T-cell receptor be
9	11	34.4	5	2	PT0281		Ig heavy chain CDR
10	11	34.4	6	2	S28637		Jacalin beta-II ch
11	11	34.4	6	2	PT0587		T-cell receptor be
12	10	31.2	5	2	S70615		endo-1,4-beta-xyla
13	10	31.2	5	2	PT0601		T-cell receptor be
14	10	31.2	6	2	PQ0008		angiotensin-conver
15	10	31.2	6	2	PT0533		T-cell receptor be
16	9	28.1	4	2	I57745		D-mannosate hydro
17	9	28.1	4	2	A41890		protein D - Escher
18	9	28.1	5	2	S62883		seminal plasma pro
19	9	28.1	5	2	PT0660		T-cell receptor be
20	9	28.1	5	2	PT0679		T-cell receptor be
21	8	25.0	4	2	I40697		biotin A - Citropa
22	8	25.0	4	2	PT0696		T-cell receptor be
23	8	25.0	5	2	A44692		fulicin - giant Af
24	8	25.0	5	2	PT0596		T-cell receptor be
25	8	25.0	5	2	PT0600		T-cell receptor be
26	8	25.0	5	2	PT0729		T-cell receptor be
27	8	25.0	5	2	PT0672		T-cell receptor be
28	8	25.0	5	2	PT0699		T-cell receptor be
29	8	25.0	5	2	PT0561		T-cell receptor be

## ALIGNMENTS

## RESULT 1

A32014

traw protein - Escherichia coli plasmid R100 (fragment)  
C:Species: Escherichia coli  
C:Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text  
C:Accession: A32014  
R:Inamoto, S.; Yoshioaka, Y.; Ohtsubo, E.  
J. Bacteriol. 170, 2749-2757, 1988  
A:Title: Identification and characterization of the pro-  
A:Reference number: A32014; MUID:88227859; PMID:28363695  
A:Accession: A32014  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <INA>  
C:Genetics:  
A:Genome: plasmid  
C:Keywords: DNA binding

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Query Match      53.1%; Score 17; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. NO. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	3	NDE	5
Dd	2	NDE	4

## RESULT 2

muscle 2  
PT0656  
T-cell receptor beta chain V-D-J region (121-1J) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0656  
R:Feenev, A.J.

Greeney, R.J.: *Exp. Med.* 174, 115-124, 1991

```
Query Match          40.6%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY	2	NNDE	5
		::	
Dp	2	SSDE	5

```

RESULT 3
PT0510
T-cell receptor beta chain V-D-J region (100-4AH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0510
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0510
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNDE 5
Db 2 SSDE 5

RESULT 4
PT0599
T-cell receptor beta chain V-D-J region (111-LAE) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0599
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0599
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNDE 5
Db 2 SSDE 5

RESULT 5
S29881
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C:Accession: S29881
R:Waelderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases around
A:Reference number: S29881; MUID:85131201; PMID:3156136
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F.4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match      40.6%; Score 13; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 NDET 6
Db 3 SDKT 6

RESULT 6
PT0573
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0573
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0573
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      37.5%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNDE 5
Db 2 SGDE 5

RESULT 7
PC4127
Hypothetical 6 protein - Streptomyces clavuligerus (fragment)
C:Species: Streptomyces clavuligerus
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PC4127
R:Rodriguez-Garcia, A.; Martin, J.F.; Liras, P.
Gene 167, 9-15, 1995
A:Title: The argG gene of Streptomyces clavuligerus has low homology to unstable argG
A:Reference number: JC4548; MUID:96144242; PMID:8566818
A:Accession: PC4127
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <ROD>
A:Cross-references: EMBL:249111

Query Match      37.5%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ND 4
Db 3 ND 4

RESULT 8
PT0650
T-cell receptor beta chain V-D-J region (121-3BF) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0650
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0650
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

```

Query Match 37.5%; Score 12; DB 2; Length 6;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NND 6  
 Db 2 SSD 6

RESULT 9  
 PT0281  
 Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0281  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0281  
 A:Molecule type: DNA  
 A:Residues: 1-5 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; Immunoglobulin

Query Match 34.4%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DE 5  
 Db 1 DE 2

RESULT 10  
 S29637  
 jacalin beta-II chain - Artocarpus champeden (fragment)  
 C:Species: Artocarpus champeden  
 C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
 C:Accession: S29637  
 R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
 Biochim. Biophys. Acta 1156, 219-222, 1993  
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
 A:Reference number: S29635; MUID:93152601; PMID:8427879  
 A:Accession: S29637  
 A:Molecule type: protein  
 A:Residues: 1-6 <NGO>  
 A:Experimental source: seed  
 C:Complex: heterotetramer; two alpha and two beta chains  
 C:Function:  
 A:Description: seed storage protein  
 A:Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine  
 C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 34.4%; Score 11; DB 2; Length 6;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDE 6  
 Db 1 NEQ 4

RESULT 11  
 PT0587  
 T-cell receptor beta chain V-D-J region (141-1BF) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0587  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0587  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <FE>  
 A:Experimental source: day 19 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 6;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NND 6  
 Db 2 SGD 6

RESULT 12  
 S70615  
 endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (frag  
 N:Alternate names: xylanase  
 C:Species: Streptomyces sp.  
 A:Variety: Chainia sp. NCL 82.5.1  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
 C:Accession: S70615  
 R:Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.  
 Biochem. J. 316, 771-775, 1996  
 A:Title: Structural environment of an essential cysteine residue of xylanase from Cha  
 A:Reference number: S70615; MUID:96265041; PMID:8670151  
 A:Accession: S70615  
 A:Molecule type: protein  
 A:Residues: 1-5 <RAO>  
 A:Experimental source: Chainia sp. strain NCL 82.5.1  
 A:Note: the source is designated as Chainia sp.  
 C:Function:  
 A:Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans  
 A:Pathway: fermentation of hemicellulose into ethanol  
 C:Keywords: glycosidase; hydrolase

Query Match 31.2%; Score 10; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ET 6  
 Db 1 ET 2

RESULT 13  
 PT0601  
 T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0601; PT0617; PT0694  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0601  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FE>  
 A:Experimental source: newborn thymus, strain BALB/c, clone 120-2K  
 A:Accession: PT0617  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FE3>  
 A:Experimental source: newborn thymus, strain BALB/c, 120-2CA  
 A:Accession: PT0694  
 A>Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-5 <FE2>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H

## C;Keywords: T-cell receptor

Query Match 31.2%; Score 10; DB 2; Length 5;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNDE 5  
 Db 2 SSDD 5

## RESULT 14

PQ0008  
 angiotensin-converting enzyme inhibitor (FLP-1) - common fig  
 N:Alternate names: ficus latex peptide 1  
 C:Species: Ficus carica (common fig)  
 C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
 C:Accession: PQ0008  
 R:Maruyama, S.; Miyoshi, S.; Tanaka, H.  
 Agric. Biol. Chem. 53, 2763-2767, 1989  
 A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
 A:Reference number: PQ0008  
 A:Accession: PQ0008  
 A:Molecule type: protein  
 A:Residues: 1-6 <HAR>  
 A:Experimental source: latex  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 31.2%; Score 10; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VN 2  
 Db 2 VN 3

## RESULT 15

PT0533  
 T-cell receptor beta chain V-D-J region (126-1AA) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0533  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0533  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <FEE>  
 A:Experimental source: adult thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 31.2%; Score 10; DB 2; Length 6;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNDE 5  
 Db 2 SSDD 5

Search completed: January 29, 2003, 10:00:00  
 Job time : 16 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:55:09 ; Search time 10 Seconds  
(without alignments)  
24.886 Million cell updates/sec

Title: US-09-878-603-15  
Perfect score: 32  
Sequence: 1 VNNDET 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	53.1	5	TRM3_ECOLI	P13973 escherichia
2	12	37.5	5	TPIS_CANFA	P54714 canis famli
3	12	37.5	6	ASP2_LACSN	P82655 lactobacilli
4	9	28.1	5	BIOA_CITFR	P13071 citrobacter
5	9	28.1	6	UN06_CLOPA	P81351 clostridium
6	7	21.9	4	EOS1_HUMAN	P02731 homo sapien
7	7	21.9	4	FLRN_ATEL	P58707 anthopleura
8	7	21.9	5	UXR4_CHLTR	P38005 chlamydia t
9	7	21.9	6	TRP1_PSEPU	P36414 pseudomonas
10	6	18.8	3	LUXE_VIBFI	P24272 vibrio fisc
11	6	18.8	4	ACH1_ACHFU	P35904 achatina fu
12	6	18.8	4	OCPL_OCTMI	P58648 octopus min
13	6	18.8	4	OCPL_OCTMI	P58649 octopus min
14	6	18.8	5	RE11_LITRU	P82070 litorea rub
15	6	18.8	6	FARP_MONEX	P41966 moniezia ex
16	6	18.8	6	TMOF_SARBU	P41495 sarcophaga
17	6	18.8	6	VP19_HSVIK	P23210 herpes simp
18	5	15.6	4	RM01_YEAST	P36515 saccharomyc
19	5	15.6	4	TUFT_HUMAN	P01858 homo sapien
20	5	15.6	5	E103_LITRU	P82099 litorea rub
21	5	15.6	5	E104_LITRU	P82100 litorea rub
22	5	15.6	5	PRCT_PERAM	P01373 periplaneta
23	5	15.6	5	PSK_DAUCA	P58261 daucus caro
24	5	15.6	5	RE21_LITRU	P82071 litorea rub
25	5	15.6	5	RE31_LITRU	P82072 litorea rub
26	5	15.6	5	RE32_LITRU	P82073 litorea rub
27	5	15.6	5	UC22_MAIZE	P80628 zea mays (m
28	5	15.6	6	ACPH_RABIT	P25154 oryctolagus
29	5	15.6	6	OVN_LEPDE	P42985 leptonotars
30	4	12.5	6	CIP1_MYTED	P13736 mytilus edu
31	4	12.5	6	CIP2_MYTED	P13737 mytilus edu
32	4	12.5	6	E101_LITRU	P82096 litorea rub
33	3	9.4	4	FYRI_ATEL	P58706 anthopleura

34 3 9.4 5 1 FARP\_ARTTR  
35 3 9.4 5 1 UF01\_MOUSE  
36 2 6.2 4 1 THYL\_PIG  
37 2 6.2 4 1 DCM\_L\_PSECH  
38 2 6.2 5 1 BIOB\_CITFR  
39 2 6.2 5 1 BPP7\_BOTIN  
40 2 6.2 6 1 LOK1\_LOCM1  
41 1 3.1 3 1 GRMM\_HUMAN  
42 1 3.1 4 1 DCM\_S\_PSECH  
43 1 3.1 4 1 FAR3\_HIRME  
44 1 3.1 4 1 FAR4\_HIRME  
45 1 3.1 4 1 FFA\_ATEL

## ALIGNMENTS

RESULT 1  
TRM3\_ECOLI  
ID TRM3\_ECOLI STANDARD; PRT; 5 AA.  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE TRAM protein (Fragment).  
GN TRAM.  
OS Escherichia coli.  
OC Plasmid IncFII R100.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88227859; PubMed=2836369;  
RA Inamoto S., Yoshioaka Y., Ohtsubo E.;  
RT "Identification and characterization of the products from the traj  
and traj genes of plasmid R100.";  
RL J. Bacteriol. 170:2749-2757(1988).  
CC - FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
CC - SUBCELLULAR LOCATION: Cytoplasmic.  
CC - SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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DR EMBL; M20941; NOT\_ANNOTATED\_CDS.  
DR PIR; A32014; A32014.  
KW Conjugation; Plasmid; DNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;  
Query Match 53.1%; Score 17; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 NDE 5  
DB 2 NDE 4  
RESULT 2  
TPIS\_CANFA  
ID TPIS\_CANFA STANDARD; PRT; 5 AA.  
AC P54714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).  
 GN TP11.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 dog heart proteins";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glycerone  
 phosphate.  
 CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.  
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 DR HSC-2DPAGE; P54714; DOG  
 DR InterPro: IPR000652; Triophos\_ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 FT Pentose shunt.  
 FT NON\_TER 1  
 FT NON\_TER 5  
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NN 3  
 DB 4 NN 5

## RESULT 3

ASP2\_LACSN  
 ID ASP2\_LACSN STANDARD; PRT; 6 AA.  
 AC P82655;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Acid shock protein 2 (Fragment).  
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1625;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CBI;  
 RX MEDLINE=21322712; PubMed=11429463;  
 RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;  
 RT "The acid-stress response in Lactobacillus sanfranciscensis CBI";  
 RL Microbiology 147:1863-1873(2001).  
 CC -!- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.  
 FT NON\_TER 6  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ND 4  
 DB 5 ND 6

## RESULT 4

BIOA\_CITFR  
 ID BIOA\_CITFR STANDARD; PRT; 5 AA.  
 AC P13071;

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase  
 DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA  
 DE aminotransferase) (Fragment).  
 GN BIOA.  
 OS Citrobacter freundii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Citrobacter.  
 OX NCBI\_TaxID=546;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89006280; PubMed=2971595;  
 RA Shiuan D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
 Citrobacter freundii and Salmonella typhimurium biotin operons";  
 RL Gene 67:203-211(1988)  
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-  
 oxononanoate -> S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-  
 diaminononanoate.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -!- PATHWAY: Biotin biosynthesis.  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 AMINOTRANSFERASES.  
 CC -----  
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 or send an email to license@sib-sib.ch).  
 CC -----  
 DR EMBL: M21922; -; NOT\_ANNOTATED\_CDS.  
 DR InterPro: IPR000954; Aminotran\_3.  
 DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
 KW Biotin biosynthesis; Transferase; Aminotransferase;  
 KW Pyridoxal phosphate.  
 FT NON\_TER 5  
 SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 5;  
 Best Local Similarity 20.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNDE 5  
 DB 1 MTDD 5

## RESULT 5

UN06\_CLOPA  
 ID UN06\_CLOPA STANDARD; PRT; 6 AA.  
 AC P81351;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Unknown protein CP 6 from 2D-page (Fragment).  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 sequence analysis of proteins from Clostridium pasteurianum W5";  
 RL Electrophoresis 19:802-806(1998).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN



```

CC PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
FT NON_TER 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDE 5
DB 2 NTAE 5

RESULT 6
EESI_HUMAN
ID EESI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
human lung tissue: identification as eosinophil chemotactic factor of
anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
(AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS) THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PIR; A03190; ETHUL.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT /FTID=VAR_005201.
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNND 4
DB 1 VGSE 4

RESULT 7
FLRN_ANGEL
ID FLRN_ANGEL STANDARD; PRT; 4 AA.
AC P58707;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS-SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asp-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group."
RT Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
KW Neuropeptide: Amidation.
FT MOD_RES 1 1 L-3-PHENYLLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 4;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNN 3
DB 2 LRN 4

RESULT 8
UXA4_CHLTR
ID UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christiane G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
DR Siena-2DPAGE; P38005;
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA80000000 CRC64;

Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NND 4
DB 2 SGD 4

RESULT 9
TRPI_PSEPU
ID TRPI_PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpBA operon transcriptional activator (Fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C15;
RX MEDLINE=89335826; PubMed=2503057;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
putida."
RL Biochimie 71:521-531(1989).
CC -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE

```

CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 CC TRAP OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X13299; CAA31560.1; -;  
 DR InterPro: IPR000847; HTH\_LysR.  
 DR PROSITE: PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;  
 Query Match 21.9%; Score 7; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 ND 4  
 DB 3 HD 4  
 RESULT 10  
 LUXE\_VIBFI STANDARD; PRT; 3 AA.  
 AC P24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-  
 DE protein synthetase) (Fragment).  
 GN LUXE.  
 OS Vibrio fischeri.  
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91072226; PubMed=2254256;  
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination  
 RT site for the lux operon."  
 RL J. Bacteriol. 172:6797-6802(1990).  
 CC -1- FUNCTION: ACRYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.  
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE  
 CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS  
 CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION  
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein -> AMP + diphosphate +  
 CC an acyl-protein thioester.  
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M62812; -; NOT\_ANNOTATED\_CDS.  
 KW Luminescence; Ligase.  
 FT NON\_TER 1  
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000000 CRC64;  
 Query Match 18.8%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 D 4  
 DB 3 D 3  
 RESULT 11  
 ACH1\_ACHFU STANDARD; PRT; 4 AA.  
 ID ACH1\_ACHFU  
 AC P35904;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Achatin-I.  
 OS Achatina fulica (Giant African snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;  
 CC Achatinacea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
 RC STRAIN=Ferussac; TISSUE=Ganglion;  
 RX MEDLINE=89273551; PubMed=2597281;  
 RA Kanatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;  
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
 RT fulica Ferussac containing a D-amino acid residue";  
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=Ferussac; TISSUE=Heart atrium;  
 RX MEDLINE=91264856; PubMed=1675568;  
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;  
 RT "Purification of achatin-I from the atria of the African giant snail,  
 RT Achatina fulica, and its possible function."  
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=93014529; PubMed=1399265;  
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
 RA Iwashita T., Nomoto K.;  
 RT "Crystal structure and molecular conformation of achatin-I  
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a  
 RT D-amino acid residue."  
 RL Int. J. Pept. Protein Res. 39:258-264(1992).  
 CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY  
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY  
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE  
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.  
 DR PIR: A32480; A32480.  
 KW Hormone; D-amino acid.  
 FT MOD\_RES 2  
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C8100000000 CRC64;  
 Query Match 18.8%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 D 4  
 DB 4 D 4  
 RESULT 12  
 OCPL\_OCTMI STANDARD; PRT; 4 AA.  
 ID OCPL\_OCTMI  
 AC P58648;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cardioactive peptides Ocp-1/Ocp-2.

OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;  
 OC Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 [1]  
 RN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RP TISSUE=Brain;  
 RC MEDLINE=20336815; PubMed=10876044;  
 RX Iwakoshi E., Hisada M., Minakata H.;  
 RA "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor";  
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less  
 CC active than Ocp-1.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD\_RES 2 2  
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;  
 Query Match 18.8%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 D 4  
 Db 4 D 4

RESULT 13  
 OCP3\_OCTMI  
 ID OCP3\_OCTMI STANDARD; PRT; 4 AA.  
 AC P58649;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;  
 OC Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 [1]  
 RN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RP TISSUE=Brain;  
 RC MEDLINE=20336815; PubMed=10876044;  
 RX Iwakoshi E., Hisada M., Minakata H.;  
 RA "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor";  
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
 CC active than Ocp-3.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD\_RES 2 2  
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 18.8%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 D 4  
 Db 4 D 4

RESULT 14  
 REIL\_LITRU  
 ID REIL\_LITRU STANDARD; PRT; 5 AA.

AC P82070;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rubellidin 1.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=Skin secretion;  
 RC Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
 CC ACTIVITY.  
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 18.8%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 D 4  
 Db 2 D 2

RESULT 15  
 FARP\_MONEX  
 ID FARP\_MONEX STANDARD; PRT; 6 AA.  
 AC P41966;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE FMRFamide-like neuropeptide GNFRF-amide.  
 OS Moniezia expansa (Sheep tapeworm).  
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 OC Cyclophyllidae; Anoplocephalidae; Moniezia.  
 OX NCBI\_TaxID=28841;  
 [1]  
 RN SEQUENCE.  
 RX MEDLINE=93312289; PubMed=8323531;  
 RA Maule A.G., Shaw C., Halton D.W., Thim L.;  
 RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from  
 RT the sheep tapeworm, Moniezia expansa";  
 RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 6 6  
 SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 18.8%; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 N 2  
 Db 2 N 2

Search completed: January 29, 2003, 09:59:04  
 Job time : 11 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:57:29 ; Search time 28 Seconds  
(without alignments)  
44,153 Million cell updates/sec

Title: US-09-878-603-15  
Perfect score: 32  
Sequence: 1 VNNDT 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	21.9	5	P83073	P83073 bacillus ce
2	6	18.8	4	Q08433	Q08433 rattus norv
3	6	18.8	5	Q99007	Q99007 hordeum vul
4	5	15.6	6	P82181	P82181 spinacia ol
5	5	15.6	6	P82541	P82541 spinacia ol
6	5	15.6	6	P82182	P82182 spinacia ol
7	1	3.1	5	P83308	P83308 gallus gall

ALIGNMENTS

RESULT 1  
P83073  
ID P83073  
AC P83073; PRELIMINARY; PRT; 5 AA.

DT 01-OCT-2001 (Tremblrel. 18, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DE 88 kDa protein (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NCIMB 11796;  
RA Browne N., Dowds B.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 21.9%; Score 7; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 6.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ET 6  
DB 3 DT 4

RESULT 2  
Q08433  
ID Q08433 PRELIMINARY; PRT; 4 AA.  
AC Q08433;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT) (Fragment).  
DE Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GUNN;  
RX MEDLINE=91282758; PubMed=1840486;  
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";  
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).  
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.  
CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR  
CC BETA-D-GLUCURONOSIDE.  
CC -!- SUBCELLULAR LOCATION: MICROSOME.  
DR EMBL: S38636; AAB19259.1;  
KW Transferase; Glycosyltransferase; Microsome; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 4  
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 18.8%; Score 6; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 N 2  
DB 1 N 1

RESULT 3  
Q99007  
ID Q99007 PRELIMINARY; PRT; 5 AA.  
AC Q99007;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).  
 GN AMYL.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;  
 RX MEDLINE-91329704; PubMed-1831055;  
 RA Jacobsen J.V., Close T.J.;  
 RT "Control of transient expression of chimaeric genes by gibberellic  
 RT acid and abscisic acid in protoplasts prepared from mature barley  
 RT aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721(1991).  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN  
 CC BARLEY.  
 DR EMBL; X54643; CAA38455.1;  
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;  
 KW Calcium; Multigene family.  
 FT NON\_TER  
 SQ SEQUENCE 5 AA; 600 MW; 6183344DD6F00000 CRC64;  
  
 Query Match 18.8%; Score 6; DB 10; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 N 2  
 DB 3 N 3  
  
 RESULT 4  
 P82181 PRELIMINARY; PRT; 6 AA.  
 ID P82181  
 AC P82181;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-CV. ALWARO; TISSUE-LEAF;  
 RX MEDLINE-20435798; PubMed-10874046;  
 RA Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the 50 S subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 275:28466-28482(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD-ELECTROSPRAY.  
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD-MALDI.  
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA  
 CC FORM IS THE MINOR BASIC FORM.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR002222; Ribosomal\_S19.  
 DR Pfam; PF00203; Ribosomal\_S19; PARTIAL.  
 DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.  
 DR PROSITE; PS00323; RIBOSOMAL\_S19; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER  
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;  
  
 Query Match 15.6%; Score 5; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 T 6  
 DB 1 T 1  
  
 RESULT 6  
 P82182 PRELIMINARY; PRT; 6 AA.  
 ID P82182  
 AC P82182;  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-CV. ALWARO; TISSUE-LEAF;  
 RX MEDLINE-20435798; PubMed-10874046;  
 RA Yamaguchi K., Subramanian A.R.;

RT The plastid ribosomal proteins. Identification of all the proteins in  
the 50 S subunit of an organelle ribosome (chloroplast).";  
RL J. Biol. Chem. 275:28466-28482(2000).  
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
DR InterPro: IPR001790; Ribosomal\_L10.  
DR InterPro: IPR002363; Ribosomal\_L10eub.  
DR Pfam: PF00466; Ribosomal\_L10; PARTIAL.  
DR PROSITE: PS01109; RIBOSOMAL\_L10; PARTIAL.  
KW Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 15.6%; Score 5; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 T 6  
DB 5 T 5

## RESULT 7

P83308  
ID P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE FMRFamide-like neuropeptide (LPLRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=BRAIN;  
RX PubMed=6137771;  
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by  
antibodies to FMRFamide.";  
RL Nature 305:328-330(1983).  
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 3.1%; Score 1; DB 13; Length 5;  
Best Local Similarity 0.0%; Pred. No. 6.7e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 V 1  
DB 1 L 1

Search completed: January 29, 2003; 09:59:38  
Job time : 28 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:54:49 ; Search time 34 Seconds  
(without alignments)  
23.515 Million cell updates/sec

Title: US-09-878-603-15  
Perfect score: 32  
Sequence: 1 VNNDT 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0  
Maximum DB seq length: 6

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	6	22 AAB74060	Human C5a peptide
2	28	87.5	6	22 AAB74068	C-terminal truncat
3	28	87.5	6	22 AAB74070	C-terminal truncat
4	26	81.2	6	22 AAB74067	C-terminal truncat
5	22	68.8	6	22 AAB74069	C-terminal truncat
6	20	62.5	6	21 AAY63421	Protocadherin cell
7	19	59.4	6	21 AAB38220	Human secreted pro
8	19	59.4	6	21 AAY63150	Li-cadherin cell ad
9	18	56.2	6	21 AAY63827	Desmoglein cell ad
10	18	56.2	6	23 AAE14592	Human interleukin-

11	18	56.2	6	23 ABB45879	Desmoglein CAR seq
12	17	53.1	4	22 AAB31513	Amino acid sequenc
13	17	53.1	5	16 AAW21375	Plasminogen activa
14	17	53.1	5	17 AAW00259	Subtilisin N62D/G1
15	17	53.1	5	18 AAW18077	Fibrinogen and cro
16	17	53.1	5	20 AAY25125	Human fibrinogen/M
17	17	53.1	5	20 AAW99136	Fg and XL-Fb alpha
18	17	53.1	5	21 AAY61941	Cadherin-12 cell a
19	17	53.1	5	21 AAY63418	Protocadherin cell
20	17	53.1	5	21 AAY63824	Desmoglein cell ad
21	17	53.1	5	22 AAB59462	Human fibrinogen a
22	17	53.1	5	23 AAO15017	Mutant VL CDR3 pep
23	17	53.1	5	23 ABB45876	Desmoglein CAR seq
24	17	53.1	6	8 AAP71386	Diuretic hexapepti
25	17	53.1	6	14 AAR41531	Pseudomonas 7A glu
26	17	53.1	6	14 AAR37077	H(+) ATPase inhibi
27	17	53.1	6	15 AAR45903	Chlamydia trachoma
28	17	53.1	6	17 AAR93979	Partial peptide fr
29	17	53.1	6	19 AAW43190	Peptide #68 tested
30	17	53.1	6	19 AAW43188	Peptide #66 tested
31	17	53.1	6	20 AAY49170	Zif268 zinc finger
32	17	53.1	6	21 AAB01537	Plasmin substrate
33	17	53.1	6	21 AAB03784	Fibrinogen alpha c
34	17	53.1	6	21 AAY61966	Cadherin-12 cell a
35	17	53.1	6	21 AAY63361	Protocadherin cell
36	17	53.1	6	23 AAB85666	Plasmin substrate
37	16	50.0	4	19 AAW79195	Nucleotide binding
38	16	50.0	4	20 AAY15821	Peptide used to ma
39	16	50.0	4	21 AAB24288	Prostate tumour as
40	16	50.0	4	21 AAY80785	Fluorophore-label
41	16	50.0	4	21 AAY61898	Cadherin-12 cell a
42	16	50.0	4	21 AAY61899	Cadherin-12 cell a
43	16	50.0	4	22 AAB82933	CEO-3 peptide subs
44	16	50.0	4	22 AAB51205	Caspase cleavage s
45	16	50.0	4	23 AAE19129	Caenorhabditis ele

#### ALIGNMENTS

RESULT 1  
AAB74060  
ID AAB74060 standard; Peptide; 6 AA.  
XX  
AC AAB74060;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE Human C5a peptide fragment #5.  
XX  
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;  
KW meningitis; respiratory; gastrointestinal; urinary tract infection;  
KW wound; anaphylatoxin; sepsis.  
XX  
OS Homo sapiens.  
XX  
PN WO200115731-A1.  
XX  
PD 08-MAR-2001.  
XX  
PF 31-AUG-2000; 2000WO-US24219.  
XX  
PR 31-AUG-1999; 99US-0387671.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Ward PA, Huber-Lang M, Sarma V;  
XX  
DR WPI: 2001-226665/23.  
DR N-PSDB: AAF75797.  
XX  
PT Compositions for treating blood-borne and toxin mediated diseases and  
PT treatment of sepsis in humans and other animals comprises anti-C5a

PT antibodies generated against C-terminal truncated C5a peptides -  
XX  
PS Claim 8; Page 26; 84pp; English.

The present sequence is a peptide fragment of human complement component C5a (the full-length sequence is given in AAB74053). The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as anaphylatoxin.

AA	Sequence	6 AA;
AA		

Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	VNND E T 6							
Db	1	VNND E S 6							
RESULT 3									
AAB74070									
ID	AAB74070 standard; Peptide; 6 AA.								
XX									
AC	AAB74070;								
XX									
DT	16-MAY-2001 (first entry)								
XX									
DE	C-terminal truncated C5a peptide #8.								
XX									
KW	C5a; complement; antibody; bacterial infection; sinusitis;								
KW	meningitis; respiratory; gastrointestinal; urinary tract infection;								
KW	wound; anaphylatoxin; sepsis.								
XX									
OS	Unidentified.								
XX									
PN	WO200115731-A1.								
XX									
PD	08-MAR-2001.								
XX									
PD	31-AUG-2000; 2000WO-US24219.								
PF									
XX									
PR	31-AUG-1999; 99US-0387671.								
XX									
PA	(UNMI ) UNIV MICHIGAN.								
XX									
XX									
PI	Ward PA, Huber-Lang M, Sarma V;								
XX									
DR	WPI; 2001-226665/23.								
XX									
PT	Compositions for treating blood-borne and toxin mediated diseases and								
PT	treatment of sepsis in humans and other animals comprises anti-C5a								
PT	antibodies generated against C-terminal truncated C5a peptides -								
XX									
PS	Disclosure; Page 29; 84pp; English.								
XX									
CC	The present sequence is a C-terminal truncated C5a peptide fragment. The								
CC	present invention relates to an antibody specific for the present								
CC	sequence. The C5a-antibody can be used in a therapeutic composition,								
CC	which is useful for treating a subject suffering from bacterial								
CC	infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or								
CC	urinary tract infections or infections in wounds. In addition, the C5a								
CC	antibody can be used for treating sepsis. C5a is also known as								
CC	anaphylatoxin.								
XX									
SQ	Sequence 6 AA;								
Query Match 87.5%; Score 28; DB 22; Length 6;									
Best Local Similarity 100.0%; Pred. No. 7.8e+05;									
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	NNND E T 6							
Db	2	NNND E T 6							
RESULT 4									
AAB74067									
ID	AAB74067 standard; Peptide; 6 AA.								
XX									
AC	AAB74067;								
XX									
DT	16-MAY-2001 (first entry)								
XX									
DE	C-terminal truncated C5a peptide #5.								
XX									



C5a; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.

Unidentified.

WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Ward PA, Huber-Lang M, Sarma V;

DR WPI; 2001-226665/23.

XX CC Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure; Page 29; 84pp; English.

XX CC The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as anaphylatoxin.

XX SQ Sequence 6 AA;

Query Match 81.2%; Score 26; DB 22; Length 6;

Best Local Similarity 83.3%; Pred. NO. 7.8e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNND6T 6

Db 1 VNNQET 6

RESULT 5

AAB74069

ID AAB74069 standard; Peptide; 6 AA.

AC AAB74069;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #7.

XX KW C5a; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.

XX OS Unidentified.

XX PN WO200115731-A1.

XX PD 08-MAR-2001.

XX PF 31-AUG-2000; 2000WO-US24219.

XX PR 31-AUG-1999; 99US-0387671.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Ward PA, Huber-Lang M, Sarma V;

XX DR

WPI; 2001-226665/23.

XX CC Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure; Page 29; 84pp; English.

XX CC The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as anaphylatoxin.

XX SQ Sequence 6 AA;

Query Match 68.8%; Score 22; DB 22; Length 6;

Best Local Similarity 66.7%; Pred. No. 7.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNND6T 6

Db 1 VNNQES 6

RESULT 6

AAY63421

ID AAY63421 standard; Peptide; 6 AA.

XX AC AAY63421;

XX DT 02-MAR-2000 (first entry)

XX DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2908.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin related neuronal receptor; Li-cadherin; protocadherin; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.

XX OS Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 1..6

FT /note= "the terminal residues are condensed with each other to form a cyclic peptide"

XX PN WO9957149-A2.

XX PD 11-NOV-1999.

XX PF 05-MAY-1999; 99WO-CA00363.

XX PR 05-MAY-1998; 98US-0073040.

XX PR 06-NOV-1998; 98US-0187859.

XX PR 20-JAN-1999; 99US-0234395.

XX PR 08-MAR-1999; 99US-0264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX DR WPI; 2000-038791/03.

XX XX

PT New cadherin modulating agents, used for modulating nonclassical  
 PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease  
 XX  
 XX  
 PS Claim 84; Page 203; 252pp; English.  
 CC  
 CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MAs can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AY60592 to AY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 62.5%; Score 20; DB 21; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VNND 5  
 DB 2 INRDE 6  
 RESULT 7  
 AAB38220  
 ID AAB38220 standard; Protein; 6 AA.  
 XX  
 AC AAB38220;  
 XX  
 XX 30-JAN-2001 (first entry)  
 DE Human secreted protein sequence encoded by gene 18 SEQ ID NO:76.  
 XX  
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; skin aging; food additive; preservative.  
 XX  
 OS Homo sapiens.  
 PN WO200058469-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 23-MAR-2000; 2000WO-US07579.  
 XX  
 PR 26-MAR-1999; 99US-0126509.  
 PR 07-JAN-2000; 2000US-0174853.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX  
 DR WPI: 2000-594542/56.  
 DR N-PSDB; AAC69472.  
 XX  
 PT Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition  
 XX  
 PS Claim 11; Page 366; 416pp; English.  
 CC  
 CC The polynucleotide sequences given in AAC69455 to AAC69502 encode the  
 CC human secreted proteins given in AAB38203 to AAB38250. AAB38251 to  
 CC AAB38320 represent human secreted polypeptide sequences and proteins  
 CC homologous to them, which are given in the exemplification of the present  
 CC invention. Human secreted proteins have activities based on the tissues  
 CC and cells the genes are expressed in. Example of activities include:  
 CC immunosuppressive; antiarthritic; antirheumatic; antiproliferative;  
 CC cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;  
 CC neuroprotective; antibacterial; virucide; fungicide; and  
 CC ophthalmological. The polynucleotides and polypeptides can be used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases, hyperproliferative disorders, cardiovascular  
 CC disorders, cerebrovascular disorders, angiogenesis, nervous system  
 CC disorders. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities. AAC69446 to AAC69454 and  
 CC AAB38202 represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 59.4%; Score 19; DB 21; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VNND 4  
 DB 1 MNND 4  
 RESULT 8  
 AAY63150  
 ID AAY63150 standard; Peptide; 6 AA.  
 XX  
 AC AAY63150;  
 XX  
 XX 02-MAR-2000 (first entry)  
 DE LI-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:2692.  
 XX  
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;  
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1..6  
 FT /note= "the terminal residues are condensed with each  
 FT other to form a cyclic peptide"

XX PN WO9957149-A2.  
 XX PD 11-NOV-1999.  
 XX PF 05-MAY-1999; 99WO-CA00363.  
 XX PR 05-MAY-1998; 98US-0073040.  
 XX PR 06-NOV-1998; 98US-0187859.  
 XX PR 20-JAN-1999; 99US-0234395.  
 XX PR 08-MAR-1999; 99US-0264516.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuk OW, Gour BJ, Byers S;  
 XX PD WPI; 2000-038791/03.  
 XX PT New cadherin modulating agents, used for modulating nonclassical  
 PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease  
 PS Claim 78; Page 199; 252pp; English.  
 XX CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MAs can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX SQ Sequence 6 AA;  
 Query Match 59.4%; Score 19; DB 21; Length 6;  
 Best Local Similarity 60.0%; Pred. NO. 7.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VNND 5  
 Db 2 INNK 6  
 RESULT 9  
 AAY63827  
 ID AAY63827 standard; Peptide; 6 AA.  
 XX AC AAY63827;  
 XX DT 02-MAR-2000 (first entry)  
 XX DE Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3279.  
 XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;

cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 cadherin related neuronal receptor; LI-cadherin; protocadherin;  
 desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 neurological disease; cyclic.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 1..6  
 FT /note= "the terminal residues are condensed with each  
 FT other to form a cyclic peptide"  
 XX PN WO9957149-A2.  
 XX PD 11-NOV-1999.  
 XX PF 05-MAY-1999; 99WO-CA00363.  
 XX PR 05-MAY-1998; 98US-0073040.  
 XX PR 06-NOV-1998; 98US-0187859.  
 XX PR 20-JAN-1999; 99US-0234395.  
 XX PR 08-MAR-1999; 99US-0264516.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuk OW, Gour BJ, Byers S;  
 XX PD WPI; 2000-038791/03.  
 XX PT New cadherin modulating agents, used for modulating nonclassical  
 PT cadherin-mediated functions for treating e.g. cancers, obesity,  
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological  
 PT disease  
 PS Claim 90; Page 209; 252pp; English.  
 XX CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MAs can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound  
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue  
 CC in a mammal. They can also be used for treating e.g. psoriasis,  
 CC arthritis, age-related macular degeneration, multiple sclerosis and  
 CC diabetes. The products can also be used for detection and diagnosis and  
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed  
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent  
 CC sequences used in the exemplification of the present invention.  
 XX SQ Sequence 6 AA;  
 Query Match 56.2%; Score 18; DB 21; Length 6;  
 Best Local Similarity 60.0%; Pred. NO. 7.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VNND 5  
 Db 2 LNKD 6

RESULT 10  
AAE14592  
ID AAE14592 standard; peptide; 6 AA.  
XX  
AC AAE14592;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human interleukin-6 helix-B.  
XX  
KW Kaposi's sarcoma-associated herpesvirus; KSHV; viral interleukin-6;  
KW vIL-6; Kaposi's sarcoma; primary effusion lymphoma; PEL;  
KW Castleman's disease; human; IL-6; helix-B.  
OS  
XX Homo sapiens.  
XX  
PN WO200210764-A2.  
XX  
PD 07-FEB-2002.  
XX  
XX 31-JUL-2001; 2001WO-US24179.  
XX  
PF  
XX  
PR 31-JUL-2000; 2000US-221719P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Aoki Y, Tosato G;  
XX  
DR WPI; 2002-206222/26.  
XX  
XX New specific binding agent that specifically binds Kaposi's sarcoma-  
PT associated herpesvirus (KSHV) interleukin-6, useful for detecting or  
PT treating Kaposi's sarcoma, primary effusion lymphoma, and Castleman's  
PT disease  
XX  
PS Example 5; Fig 4; 88pp; English.  
XX  
CC The invention relates to a specific binding agent that specifically binds  
CC Kaposi's sarcoma-associated herpesvirus (KSHV) interleukin-6 (vIL-6)  
CC and neutralises the activity of vIL-6. The specific binding agent  
CC of the invention is useful for detecting or treating a KSHV-associated  
CC disorder including Kaposi's sarcoma, primary effusion lymphoma (PEL),  
CC and Castleman's disease and for determining the prognosis of a  
CC KSHV-associated disorder. The present sequence is human IL-6  
CC helix-B fragment used in an exemplification of the invention.  
XX  
SQ Sequence 6 AA;  
Query Match 56.2%; Score 18; DB 23; Length 6;  
Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 NDET 6  
DB 2 NEET 5  
RESULT 11  
ABB45879  
ID ABB45879 standard; Peptide; 6 AA.  
XX  
AC ABB45879;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE Desmoglein CAR sequence cyclic peptide SEQ ID NO 623.  
XX  
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;  
KW skin graft; organ implant; autoimmune blistering disorder; cancer;  
KW apoptosis; cyclic.  
XX  
OS Synthetic.

XX WO200172956-A2.  
PN  
XX  
PD 04-OCT-2001.  
XX  
XX 27-MAR-2001; 2001WO-IB01400.  
PF  
XX  
PR 27-MAR-2000; 2000US-0535852.  
XX  
XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
PA  
XX Blaschuk OW, Symonds JM, Gour BJ;  
PI  
XX WPI; 2002-025778/03.  
DR  
XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis -  
XX  
PS Claim 18; Page 99; 127pp; English.  
XX  
CC The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer  
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.  
XX  
SQ Sequence 6 AA;  
Query Match 56.2%; Score 18; DB 23; Length 6;  
Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VNDE 5  
DB 2 LNKDE 6  
RESULT 12  
AAB31513  
ID AAB31513 standard; peptide; 4 AA.  
XX  
AC AAB31513;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Amino acid sequence of a preptin peptide fragment.  
XX  
KW Bioactive peptide; preptin; pancreatic islet beta-cell;  
KW glucose-mediated insulin secretion; insulin synthesis; type II diabetes;  
KW glucose mediated insulin secretion.  
XX  
OS Synthetic.  
XX  
PN WO200078805-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 19-JUN-2000; 2000WO-NZ00102.  
XX  
PR 18-JUN-1999; 99NZ-0336359.  
XX  
PA (COOP/) COOPER G J S.  
PA (BUCH/) BUCHANAN C M.  
XX

PI Cooper GJS, Buchanan CM;  
 XX WPI; 2001-112313/12.  
 XX  
 PT New mammalian peptide with preptin functionality, useful for preventing  
 PT or treating Type 2 diabetes mellitus by stimulating insulin secretion -  
 XX  
 PS Disclosure; Page 8; 51pp; English.  
 XX  
 CC AAB31512-AAB31514 represent fragments of a preptin. Preptin is  
 CC secreted by pancreatic islet beta-cells which enhances glucose-mediated  
 CC insulin secretion. Preptin peptides and their analogues are useful in  
 CC preparing medicaments for preventing or treating a condition which  
 CC results in or involves deficient insulin synthesis, secretion or action  
 CC e.g. type II diabetes. Antibodies specific to preptin peptides are useful  
 CC in an immunological assay such as radioimmunoassay (RIA), IRMA  
 CC (undefined) or Enzyme linked immunosorbent assay (ELISA) for  
 CC quantitatively measuring preptin in a biological fluid preferably in  
 CC cerebrospinal fluid. Agonists or antagonists of preptin peptides are  
 CC useful for modulating glucose mediated insulin secretion.  
 XX  
 SQ Sequence 4 AA;  
 Query Match 53.1%; Score 17; DB 22; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 NDE 5  
 DB 1 NDE 3  
 RESULT 13  
 AAW21375  
 ID AAW21375 standard; peptide; 5 AA.  
 XX AC AAW21375;  
 XX  
 DT 29-JUL-1997 (first entry)  
 XX  
 DE Plasminogen activator inhibitor 1 derived signal oligopeptide #3.  
 XX  
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
 KW fibroblast WPI1; schistosoma elastase precursor; schistosomin;  
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9519568-A1.  
 XX  
 PD 20-JUL-1995.  
 XX  
 PF 12-JAN-1995; 95WO-US00575.  
 XX  
 PR 14-JAN-1994; 94US-0182248.  
 XX  
 PA (RATH/) RATH M.  
 XX  
 PI Rath M;  
 XX  
 DR WPI; 1995-263953/34.  
 XX  
 XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between protein(s)

XX Claim 5; Page 52; 88pp; English.  
 PS  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 53.1%; Score 17; DB 16; Length 5;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 NNDE 5  
 DB 2 NKDE 5  
 RESULT 14  
 AAW00259  
 ID AAW00259 standard; Peptide; 5 AA.  
 XX AC AAW00259;  
 XX  
 DT 16-DEC-1996 (first entry)  
 XX  
 DE Subtilisin N2D/G166D protease-resistant peptide.  
 XX  
 KW Subtilisin BPN'; protease; enzyme engineering; protein engineering;  
 KW Bacillus amyloliquefaciens; mutagenesis; substrate specificity;  
 KW phage display.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9627671-A1.  
 XX  
 PD 12-SEP-1996.  
 XX  
 PF 27-FEB-1996; 96WO-US02861.  
 XX  
 PR 19-JUL-1995; 95US-0504265.  
 XX  
 PR 03-MAR-1995; 95US-0398028.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ballinger MD, Wells JA;  
 XX  
 DR WPI; 1996-425431/42.  
 XX  
 PT Subtilisin variants for cleaving substrates contg. basic residues -  
 PT allow effective cleavage of fusion proteins with basic linker  
 PT sequences  
 XX  
 PS Example 4; Page 27; 83pp; English.  
 XX  
 CC A phage display system was used to screen 5-residue substrate  
 CC linkers for cleavage by subtilisin BPN' N62D/G166D double mutant  
 CC (AAW00247). The library was subjected to 9 rounds of selection, and  
 CC clones that were increasingly sensitive or resistant to cleavage

CC were selected. Of 10 clones sequenced from the resistant pool, 7  
 CC contained no basic sites (AAW00254-60), 2 were monobasic (AAW00261-62)  
 CC and 1 contained 2 basic sites (AAW00263); these basic sites were all  
 CC followed by a Pro residue at position P1'. In the sensitive pool,  
 CC 3 clones were monobasic (AAW00248) and 18 were dibasic (AAW00249-53).  
 CC The NG2D/G166D double mutant specifically cleaves protein  
 CC substrates contg. basic amino acid residues at positions P1 and P2.  
 XX

SQ Sequence 5 AA;

Query Match 53.1%; Score 17; DB 17; Length 5;  
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4

DB 1 VNNN 4

# RESULT 15

AAW18077

ID AAW18077 standard; peptide: 5 AA.

XX AC AAW18077;

XX DT 07-AUG-1997 (first entry)

XX DE Fibrinogen and cross-linked fibrin alpha-chain digest.

XX KW Matrix metalloproteinase; MMP; matrixin; Fg; XL-Fb; FMP;

XX KW fibrinolytic metalloproteinase; thrombolytic therapy; reocclusion;

XX KW restenosis; atherosclerotic plaque.

XX OS Homo sapiens.

XX PN WO9636227-A1.

XX PD 21-NOV-1996.

XX PF 17-MAY-1996; 96WO-US07188.

XX PR 17-MAY-1995; 95US-0446887.

XX PA (NYBL-) NEW YORK BLOOD CENT INC.

XX PI Bini A;

XX DR WPI; 1997-011748/01.

XX PT Degradation of fibrin and fibrinogen with metallo:proteinase, esp.

XX PT MMP3 - partic. to prevent re-occlusion or restenosis and

XX PT atherosclerotic plaque

XX PS Example 10; Page 33; 57pp; English.

XX CC The present sequence is a alpha-chain NH2-terminal sequence obtained by

XX CC digestion of fibrinogen (Fg) and cross-linked fibrin (XL-Fb) by matrix

XX CC metalloproteinase-3 (MMP-3). This indicates that MMP-3 cleaves both

XX CC Fg and XL-Fb at the position corresponding to alpha103. In vivo

XX CC treatment with MMP is used following thrombolytic therapy to inhibit

XX CC reocclusion; following surgery to inhibit restenosis and to inhibit

XX CC formation (or promote regression) of atherosclerotic plaque. MMP can

XX CC also be used diagnostically (in vitro) to characterise Fb and Fg (from

XX CC their degradation products) and to coat medical equipment. More

XX CC generally, fibrinolysis can be regulated by somatic cell gene transfer

XX CC therapy to increase/decrease activity or expression of endogenous MMP.

XX SQ Sequence 5 AA;

Query Match

Best Local Similarity 53.1%; Score 17; DB 18; Length 5;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDNT 6  
 DB 1 NRNDNT 5

Search completed: January 29, 2003, 09:58:47  
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:59:45 ; Search time 10 Seconds  
(without alignments)  
12.107 Million cell updates/sec

Title: US-09-878-603-15

Perfect score: 32

Sequence: 1 VNND6T 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 6164

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	28	87.5	6	9	US-09-878-603-25
3	28	87.5	6	9	US-09-878-603-27
4	26	81.2	6	9	US-09-878-603-24
5	22	68.8	6	9	US-09-878-603-26
6	19	59.4	6	9	US-09-211-424-22
7	18	56.2	6	10	US-09-784-810A-25
8	17	53.1	4	10	US-09-784-810A-18
9	17	53.1	5	10	US-09-817-661-33
10	17	53.1	6	10	US-09-784-810A-26
11	16	50.0	4	10	US-09-947-387-4
12	16	50.0	5	10	US-09-947-387-5
13	16	50.0	6	9	US-09-884-767A-208
14	15	46.9	4	10	US-09-071-838-231
15	15	46.9	6	10	US-09-854-799-50
16	14	43.8	6	10	US-09-725-735A-23
17	14	43.8	6	12	US-10-100-057-1
18	13	40.6	4	9	US-09-953-639C-11
19	13	40.6	4	10	US-09-782-980-105

20	13	40.6	4	10	US-09-982-172-6	Sequence 6, Appli
21	13	40.6	5	10	US-09-898-461-12	Sequence 12, Appli
22	13	40.6	5	10	US-09-898-461-13	Sequence 13, Appli
23	13	40.6	6	9	US-09-987-457-3	Sequence 3, Appli
24	13	40.6	6	10	US-09-725-735A-22	Sequence 22, Appli
25	13	40.6	6	10	US-09-935-297-64	Sequence 64, Appli
26	13	40.6	6	12	US-10-136-820-96	Sequence 96, Appli
27	12	37.5	3	10	US-09-853-918-1	Sequence 1, Appli
28	12	37.5	4	8	US-08-450-842-89	Sequence 89, Appli
29	12	37.5	4	9	US-10-029-191-10	Sequence 10, Appli
30	12	37.5	4	9	US-10-029-191-17	Sequence 17, Appli
31	12	37.5	4	9	US-09-896-594-1	Sequence 1, Appli
32	12	37.5	4	9	US-10-029-301-10	Sequence 10, Appli
33	12	37.5	4	9	US-10-061-395-36	Sequence 36, Appli
34	12	37.5	4	9	US-10-098-514-19	Sequence 19, Appli
35	12	37.5	4	9	US-10-215-297-21	Sequence 21, Appli
36	12	37.5	4	9	US-09-925-803-4	Sequence 4, Appli
37	12	37.5	4	9	US-10-207-951-13	Sequence 13, Appli
38	12	37.5	4	9	US-10-215-298-21	Sequence 21, Appli
39	12	37.5	4	10	US-09-854-122-3	Sequence 3, Appli
40	12	37.5	4	10	US-09-347-064-36	Sequence 36, Appli
41	12	37.5	4	10	US-09-989-789-4084	Sequence 4084, Ap
42	12	37.5	4	10	US-09-737-255-6	Sequence 6, Appli
43	12	37.5	4	10	US-09-333-527-4	Sequence 4, Appli
44	12	37.5	4	10	US-09-784-810A-24	Sequence 24, Appli
45	12	37.5	4	10	US-09-781-804-3	Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-878-603-15  
; Sequence 15, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czerniak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis  
; FILE REFERENCE: JM-03783  
; CURRENT APPLICATION NUMBER: US/09/878,603  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: 09/387,671  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-878-603-15

Query Match 100.0%; Score 32; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND6T 6

DB 1 VNND6T 6

##### RESULT 2

US-09-878-603-25  
; Sequence 25, Application US/09878603  
; Patent No. US20020165138A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Peter A.  
; APPLICANT: Huber-Lang, Markus  
; APPLICANT: Sarma, Vidya  
; APPLICANT: Czerniak, Boris  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis

```
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-25

Query Match      87.5%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNNDDET 6
Db 1 VNNDDE 6

RESULT 3
US-09-878-603-27
; Sequence 27, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-27

Query Match      87.5%; Score 28; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NNDET 6
Db 2 NNDET 6

RESULT 4
US-09-878-603-24
; Sequence 24, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
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; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-24

Query Match      81.2%; Score 26; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNNDDET 6
Db 1 VNNDDET 6

RESULT 5
US-09-878-603-26
; Sequence 26, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-26

Query Match      68.8%; Score 22; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNNDDET 6
Db 1 VNNDDET 6

RESULT 6
US-09-211-424-22
; Sequence 22, Application US/09211424A
; Patent No. US2002017231A1
; GENERAL INFORMATION:
; APPLICANT: Staunton et al.
; TITLE OF INVENTION: Leupaxin Materials and Methods
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/211,424A
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-211-424-22

Query Match      59.4%; Score 19; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 NNDET 6  
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Db 1 NLDET 5

RESULT 7  
US-09-784-810A-25  
; Sequence 25, Application US/09784810A  
; Patent No. US20020082203A1  
; GENERAL INFORMATION:  
; APPLICANT: RASTEELI, LUCA  
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: 10716-08  
; CURRENT APPLICATION NUMBER: US/09/784,810A  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,360  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/191,261  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: motif  
US-09-784-810A-25

Query Match 56.2%; Score 18; DB 10; Length 6;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNDE 5  
| | | |  
Db 1 SNDE 4

RESULT 8  
US-09-784-810A-18  
; Sequence 18, Application US/09784810A  
; Patent No. US20020082203A1  
; GENERAL INFORMATION:  
; APPLICANT: RASTEELI, LUCA  
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: 10716-08  
; CURRENT APPLICATION NUMBER: US/09/784,810A  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,360  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/191,261  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: motif  
US-09-784-810A-18

Query Match 53.1%; Score 17; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDE 5  
| | |

Db 1 NDE 3

RESULT 9  
US-09-817-661-33  
; Sequence 33, Application US/09817661  
; Patent No. US20020076692A1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane  
; APPLICANT: Hollet, Thor  
; TITLE OF INVENTION: Improvements to ribosome display  
; FILE REFERENCE: 84633  
; CURRENT APPLICATION NUMBER: US/09/817,661  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/193,802  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Mutagenized  
; OTHER INFORMATION: sequence  
US-09-817-661-33

Query Match 53.1%; Score 17; DB 10; Length 5;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
| | | |  
Db 2 VNND 5

RESULT 10  
US-09-784-810A-26  
; Sequence 26, Application US/09784810A  
; Patent No. US20020082203A1  
; GENERAL INFORMATION:  
; APPLICANT: RASTEELI, LUCA  
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: 10716-08  
; CURRENT APPLICATION NUMBER: US/09/784,810A  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 60/182,360  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 60/191,261  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: motif  
US-09-784-810A-26

Query Match 53.1%; Score 17; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDE 5  
| | | |  
Db 1 NDE 3

RESULT 11  
US-09-947-387-4

; Sequence 4, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: NO. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-947-387-4

Query Match 50.0%; Score 16; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DET 6  
Db 1 DET 3

RESULT 12  
US-09-947-387-75  
; Sequence 75, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: NO. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

US-09-947-387-75  
Query Match 50.0%; Score 16; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 DET 6  
Db 1 DET 3  
RESULT 13  
US-09-884-767A-208  
; Sequence 208, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C.  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 208  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic enterokinase cleavage sequence  
US-09-884-767A-208

Query Match 50.0%; Score 16; DB 9; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VNND 4  
Db 2 INDD 5  
RESULT 14  
US-09-071-838-231  
; Sequence 231, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadevari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,838  
FILING DATE: 01-MAY-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-086100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-071-838-231

Query Match 46.9%; Score 15; DB 10; Length 4;  
Best Local Similarity 66.7%; Pred. No. le+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNN 3  
Db 1 INN 3

RESULT 15  
US-09-854-799-50  
Sequence 50, Application US/09854799  
Patent No. US20020115064A1  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham, Corporation  
TITLE OF INVENTION: Recombinant Feline Coronavirus S  
Proteins  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,799  
FILING DATE: 14-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,459  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/613,066  
FILING DATE: 14-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: King, William T.  
REGISTRATION NUMBER: 30,954  
REFERENCE/DOCKET NUMBER: SBC 14532B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5015  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-854-799-50

Query Match 46.9%; Score 15; DB 10; Length 6;  
Best Local Similarity 66.7%; Pred. No. le+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNN 3  
Db 4 INN 6

Search completed: January 29, 2003, 10:03:21  
Job time : 10 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 29, 2003, 09:58:09 ; Search time 13 Seconds  
(without alignments)  
13.580 Million cell updates/sec

Title: US-09-878-603-15

Perfect score: 32

Sequence: 1 VNNDET 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 32749

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2.6/pdata/1/1aa/6A-COMB.pep.\*  
4: /cgn2.6/pdata/1/1aa/6B-COMB.pep.\*  
5: /cgn2.6/pdata/1/1aa/6C-COMB.pep.\*  
6: /cgn2.6/pdata/1/1aa/6D-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	19	59.4	6	4	US-09-187-859-2692
3	18	56.2	6	4	US-08-895-590-100
4	18	56.2	6	4	US-09-187-859-3279
5	18	56.2	6	5	PCT-US94-01321-59
6	17	53.1	5	1	US-08-460-343B-48
7	17	53.1	5	1	US-08-398-028B-48
8	17	53.1	5	2	US-08-504-265B-48
9	17	53.1	5	2	US-08-765-815-5
10	17	53.1	5	3	US-08-859-738A-5
11	17	53.1	5	4	US-09-187-859-1752
12	17	53.1	5	4	US-09-187-859-2905
13	17	53.1	5	4	US-09-187-859-3276
14	17	53.1	6	2	US-08-374-560-33
15	17	53.1	6	4	US-09-187-859-1751
16	17	53.1	6	4	US-09-187-859-2845
17	16	50.0	4	4	US-09-357-952-4
18	16	50.0	4	4	US-09-521-650-4
19	16	50.0	4	4	US-09-168-888-4
20	16	50.0	4	4	US-09-187-859-253
21	16	50.0	4	4	US-09-187-859-254
22	16	50.0	5	1	US-08-335-198-13
23	16	50.0	5	1	US-08-405-200-8
24	16	50.0	5	1	US-08-405-200-9
25	16	50.0	5	4	US-09-070-637-9
26	16	50.0	5	4	US-09-521-650-75
27	16	50.0	5	4	US-09-168-888-75

28	16	50.0	5	4	US-09-187-859-255	Sequence 255, App
29	16	50.0	5	4	US-09-187-859-256	Sequence 256, App
30	16	50.0	5	4	US-09-187-859-258	Sequence 258, App
31	16	50.0	5	4	US-09-187-859-1736	Sequence 1736, Ap
32	16	50.0	5	4	US-09-187-859-1757	Sequence 1757, Ap
33	16	50.0	5	4	US-09-187-859-1762	Sequence 1762, Ap
34	16	50.0	5	4	US-09-187-859-1778	Sequence 1778, Ap
35	16	50.0	5	4	US-09-187-859-1780	Sequence 1780, Ap
36	16	50.0	5	4	US-09-187-859-1782	Sequence 1782, Ap
37	16	50.0	5	4	US-09-187-859-2689	Sequence 2689, Ap
38	16	50.0	5	4	US-09-646-154-12	Sequence 12, Appl
39	16	50.0	6	1	US-08-405-200-4	Sequence 4, Appl
40	16	50.0	6	2	US-08-374-560-34	Sequence 34, Appl
41	16	50.0	6	2	US-08-374-560-35	Sequence 35, Appl
42	16	50.0	6	2	US-08-482-228-67	Sequence 67, Appl
43	16	50.0	6	3	US-08-482-528-67	Sequence 67, Appl
44	16	50.0	6	4	US-09-187-859-257	Sequence 257, App
45	16	50.0	6	4	US-09-187-859-259	Sequence 259, App

#### ALIGNMENTS

RESULT 1  
US-09-187-859-2903  
; Sequence 2908, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2908  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence  
US-09-187-859-2908

Query Match 62.5%; Score 20; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNNDE 5  
: : : :  
Db 2 INRDE 6

RESULT 2  
US-09-187-859-2692  
; Sequence 2692, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2692  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: LI-cadherin cell adhesion recognition sequence  
US-09-187-859-2692

Query Match 59.4%; Score 19; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNND 5  
Db 2 INNKE 6

RESULT 3  
US-08-895-590-100  
Sequence 100, Application US/08895590  
Patent No. 6207410  
GENERAL INFORMATION:  
APPLICANT: Hall, Linda M.  
APPLICANT: Ren, Dejian  
APPLICANT: Zheng, Wei  
APPLICANT: Dubald, Manuel Marcel Paul  
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/895,590  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/374,888  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McGowan, Malcolm M.  
REGISTRATION NUMBER: 39,300  
REFERENCE/DOCKET NUMBER: 022650-263  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6207410 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 6  
OTHER INFORMATION: /note= "inosine"

Query Match 56.2%; Score 18; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NND 4  
Db 1 NND 3

RESULT 4  
US-09-187-859-3279  
Sequence 3279, Application US/09187859A  
Patent No. 6358920  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
FILE REFERENCE: 100086.407C1  
CURRENT APPLICATION NUMBER: US/09/187,859A  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 4052  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3279  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Representative cyclic modulating agent based on  
OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3279

Query Match 56.2%; Score 18; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNND 5  
Db 2 LNKDE 6

RESULT 5  
PCT-US94-01321-59  
Sequence 59, Application PC/TUS9401321  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Altered Linolenic and Linoleic acid Content  
TITLE OF INVENTION: In Plants  
NUMBER OF SEQUENCES: 72  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01321  
FILING DATE: 04-FEB-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156551  
FILING DATE: 22-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/014431  
FILING DATE: 05-FEB-1993  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-01321-59

Query Match 56.2%; Score 18; DB 5; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NDET 6  
Db 2 NDES 5

RESULT 6

US-08-460-343B-48  
; Sequence 48, Application US/08460343B  
; Patent No. 5741664  
; GENERAL INFORMATION:  
; APPLICANT: Marcus D. Ballinger and James A. Wells  
; TITLE OF INVENTION: SUBSTITISIN VARIANTS CAPABLE OF CLEAVING  
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,343B  
; FILING DATE: 01-Jun-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398028  
; FILING DATE: 03-mar-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0936C1  
; TELEPHONE: 650/225-8228  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-460-343B-48

Query Match 53.1%; Score 17; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
|||:  
Db 1 VNND 4

RESULT 7  
US-08-398-028B-48  
; Sequence 48, Application US/08398028B  
; Patent No. 5780285  
; GENERAL INFORMATION:  
; APPLICANT: Marcus D. Ballinger and James A. Wells  
; TITLE OF INVENTION: SUBSTITISIN VARIANTS CAPABLE OF CLEAVING  
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398,028B

Query Match 53.1%; Score 17; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
|||:  
Db 1 VNND 4

; FILING DATE: 03-Mar-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0936  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-398-028B-48

Query Match 53.1%; Score 17; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
|||:  
Db 1 VNND 4

RESULT 8  
US-08-504-265B-48  
; Sequence 48, Application US/08504265B  
; Patent No. 5837516  
; GENERAL INFORMATION:  
; APPLICANT: Marcus D. Ballinger and James A. Wells  
; TITLE OF INVENTION: SUBSTITISIN VARIANTS CAPABLE OF CLEAVING  
; TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504,265B  
; FILING DATE: 19-Jul-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398028  
; FILING DATE: 03-Mar-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0936P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-504-265B-48

Query Match 53.1%; Score 17; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
|||:  
Db 1 VNND 4

US-08-504-265B-48  
; Sequence 48, Application US/08504265B  
; Patent No. 5837516  
; GENERAL INFORMATION:  
; APPLICANT: Marcus D. Ballinger and James A. Wells  
; TITLE OF INVENTION: SUBSTITISIN VARIANTS CAPABLE OF CLEAVING  
; TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504,265B  
; FILING DATE: 19-Jul-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398028  
; FILING DATE: 03-Mar-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0936P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-504-265B-48

Query Match 53.1%; Score 17; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNND 4  
|||:  
Db 1 VNND 4

Db 1 VNN 4

RESULT 9  
US-08-765-815-5  
; Sequence 5, Application US/08765815  
; Patent No. 592322  
; GENERAL INFORMATION:  
; APPLICANT: Bini, Alessandra  
; TITLE OF INVENTION: FIBRIN(OGEN) DEGRADATION BY FIBRINOLYTIC  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,815  
; FILING DATE: 17-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/07188  
; FILING DATE: 17-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: tran, Jessica H.  
; REGISTRATION NUMBER: 40,846  
; REFERENCE/DOCKET NUMBER: 454-6 CIP/PCT/USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-765-815-5

Query Match 53.1%; Score 17; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2e+05; 2; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDET 6  
| | |  
Db 1 NRNT 5

RESULT 10  
US-08-859-738A-5  
; Sequence 5, Application US/08859738A  
; Patent No. 6020181  
; GENERAL INFORMATION:  
; APPLICANT: Bini, Alessandra  
; TITLE OF INVENTION: INHIBITION OF THROMBUS FORMATION BY MEDICAL  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753

Query Match 53.1%; Score 17; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2e+05; 2; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDET 6  
| | |  
Db 1 NRNT 5

RESULT 11  
US-09-187-859-1752  
; Sequence 1752, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753

Query Match 53.1%; Score 17; DB 3; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2e+05; 2; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDET 6  
| | |  
Db 1 NRNT 5

RESULT 12  
US-09-187-859-2905  
; Sequence 2905, Application US/09187859A

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,738A  
; FILING DATE: 17-MAY-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,887  
; FILING DATE: 17-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ronald J. Baron  
; REGISTRATION NUMBER: 29,281  
; REFERENCE/DOCKET NUMBER: 454-6 CIP II  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-859-738A-5

Query Match 53.1%; Score 17; DB 3; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2e+05; 2; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNDET 6  
| | |  
Db 1 NRNT 5

RESULT 11  
US-09-187-859-1752  
; Sequence 1752, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753

Query Match 53.1%; Score 17; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2e+05; 1; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NNDET 6  
| | |  
Db 1 DDET 4

RESULT 12  
US-09-187-859-2905  
; Sequence 2905, Application US/09187859A

```
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2905
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2905

Query Match 53.1%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 NNDE 5
Db 2 NRDE 5

RESULT 13
US-09-187-859-3276
; Sequence 3276, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3276
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3276

Query Match 53.1%; Score 17; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 2 NNDE 5
Db 2 NKDE 5

RESULT 14
US-08-374-560-33
; Sequence 33, Application US/08374560
; Patent No. 5882645
; GENERAL INFORMATION:
; APPLICANT: TOTU, Istvan
; APPLICANT: GIBBONS, William Anthony
; TITLE OF INVENTION: PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
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; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,560
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9215780.9
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/365-302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-374-560-33

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Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VNNDCT 6
Db 1 LQNDCT 6

RESULT 15
US-09-187-859-1751
; Sequence 1751, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1751
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-187-859-1751

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Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NNDET 6
Db 1 DDET 4
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Wed Jan 29 09:45:13 2003

us-09-878-603-15.closed.ra1

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Search completed: January 29, 2003, 10:00:21  
Job time : 14 secs